

xx Heston MDW, O'Keefe DS:
 xx WPI: 2000-679461/66.
 DR P-PSDB: AAB19377.
 xx
 PT New DNA fragment encoding mammalian prostate specific membrane antigen
 PT (PSMA) like protein, useful for distinguishing mammalian PSMA gene
 PT expression or protein from PSMA-like gene expression or protein
 xx
 PS Claim 2; Page 56-57; 75pp; English.
 xx
 CC The present sequence encodes a human prostate specific membrane
 CC antigen (PSMA) like protein. The PSMA-like gene is mapped to chromosome
 CC 11q14.3, to the schizophrenia disorder type II locus. Antibodies
 CC directed against PSMA-like protein are useful for diagnosing cancers
 CC (prostate, bladder, pancreatic, sarcoma, melanoma, lung or kidney) or
 CC neurological disorders such as schizophrenia. They may also be used
 CC for screening for ligands of PSMA-like protein and imaging cells
 CC expressing PSMA-like protein.
 CC
 SQ Sequence 1992 BP; 638 A; 352 C; 451 G; 551 T; 0 other;

Query Match 100.0%; Score 1992; DB 21; Length 1992;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCAATCTCTACATACCAATTAAGACATTTCCAAATCTGATGTTGAGATTTTGA 60
 DB 1 AGCAATCTCTACATACCAATTAAGACATTTCCAAATCTGATGTTGAGATTTTGA 60
 OY 61 GAGCTTATAGTAGCAAAAAAGAAAGGAAATTCCTCTGAGATGCTTTTGTAGGCC 120
 DB 61 GAGCTTATAGTAGCAAAAAAGAAAGGAAATTCCTCTGAGATGCTTTTGTAGGCC 120
 OY 121 TAATGACAAAAGTTGAAGATTAAGTTCTAGTACTATTAAAGTAAATTAATGAAATG 180
 DB 121 TAATGACAAAAGTTGAAGATTAAGTTCTAGTACTATTAAAGTAAATTAATGAAATG 180
 OY 181 ATATTACCAATCTGGAACAACAATTTAAATTAAGAAAGAAAGACACTGTGTTTCTA 240
 DB 181 ATATTACCAATCTGGAACAACAATTTAAATTAAGAAAGAAAGACACTGTGTTTCTA 240
 OY 241 GGTAAAAATGCCAGCTGSCAGGGGGCCAAAGAGTCTTCTACTCAGACCCGTGTA 300
 DB 241 GGTAAAAATGCCAGCTGSCAGGGGGCCAAAGAGTCTTCTACTCAGACCCGTGTA 300
 OY 301 CTACTTGTCTCTGGGGTGAAGTCTTATCCAGAGCTTGAATCTTCTGAGGTGCTGT 360
 DB 301 CTACTTGTCTCTGGGGTGAAGTCTTATCCAGAGCTTGAATCTTCTGAGGTGCTGT 360
 OY 361 CCAGCGTGAATATCTTAATCTGAATGTGTCAGAGAGACCTCTCACCAGGTTACCC 420
 DB 361 CCAGCGTGAATATCTTAATCTGAATGTGTCAGAGAGACCTCTCACCAGGTTACCC 420
 OY 421 AGCAATGAATACGCTTATAGCATGAATTCAGAGGCTGTGGTCTTCCAAGTATTC 480
 DB 421 AGCAATGAATACGCTTATAGCATGAATTCAGAGGCTGTGGTCTTCCAAGTATTC 480
 OY 481 TGTTCATCCAGTGGATCTATGATGCAAGAGCTCTTAAAAAAAGGGTGGCTCAGC 540
 DB 481 TGTTCATCCAGTGGATCTATGATGCAAGAGCTCTTAAAAAAAGGGTGGCTCAGC 540
 OY 541 ACCACAGATAGCAGCTGAGAGAGAGCTCAAAAGTGTCTACAAATGTTGACCTGGCTT 600
 DB 541 ACCACAGATAGCAGCTGAGAGAGAGCTCAAAAGTGTCTACAAATGTTGACCTGGCTT 600
 OY 601 TACTGGAATCTTTCTACACAAAAAGTCAAGATGCATCCACTCTACCAATGAAGTAC 660
 DB 601 TACTGGAATCTTTCTACACAAAAAGTCAAGATGCATCCACTCTACCAATGAAGTAC 660
 OY 661 GAGATTTTACAAATGTGATGCTCTCAGAGAGAGCTGACACAGATATGTTCAT 720
 DB 661 GAGATTTTACAAATGTGATGCTCTCAGAGAGAGCTGACACAGATATGTTCAT 720

DB 661 GAGATTTTACAAATGTGATGCTCTCAGAGAGAGCTGACACAGATATGTTCAT 720
 OY 721 TCTGGAGAGTACCGGGACCTCATGGATGGTGTGATTTGATGACCCCTGAGATGAGCAGC 780
 DB 721 TCTGGAGAGTACCGGGACCTCATGGATGGTGTGATTTGATGATGACCCCTGAGATGAGCAGC 780
 OY 781 TGTGTTTCATGAACCTGTGAGAGCTTTTGAACACTGAAGAAAGAGGAGGAGACCTAG 840
 DB 781 TGTGTTTCATGAACCTGTGAGAGCTTTTGAACACTGAAGAAAGAGGAGGAGACCTAG 840
 OY 841 AAGAACATTTTGTTCACAGCTGGCATGCCAAGAAATTTGCTTCTGCTTCTACTGA 900
 DB 841 AAGAACATTTTGTTCACAGCTGGCATGCCAAGAAATTTGCTTCTGCTTCTACTGA 900
 OY 841 AAGAACATTTTGTTCACAGCTGGCATGCCAAGAAATTTGCTTCTGCTTCTACTGA 900
 DB 841 AAGAACATTTTGTTCACAGCTGGCATGCCAAGAAATTTGCTTCTGCTTCTACTGA 900
 OY 901 GTGGCGAGAGATTAATCAAGACTCTTCAAGACGCGGCGGTCTATATTAATGCTGA 960
 DB 901 GTGGCGAGAGATTAATCAAGACTCTTCAAGACGCGGCGGTCTATATTAATGCTGA 960
 OY 961 CTGATCTATAGAAAGAACTACACTGAGAGTGTGATTTGATACACCACTGATGTACAGCTT 1020
 DB 961 CTGATCTATAGAAAGAACTACACTGAGAGTGTGATTTGATACACCACTGATGTACAGCTT 1020
 OY 1021 GGTATACACCTACAAAGAGCTGAAGAGCCCTGATGAAGGCTTTGAAGCAATCTCT 1080
 DB 1021 GGTATACACCTACAAAGAGCTGAAGAGCCCTGATGAAGGCTTTGAAGCAATCTCT 1080
 OY 1081 TTATGAAGTTGACCTTAAAGAAAGTCCCTCCAGAGTTCAGTGGCATGCGCAGATTAAG 1140
 DB 1081 TTATGAAGTTGACCTTAAAGAAAGTCCCTCCAGAGTTCAGTGGCATGCGCAGATTAAG 1140
 OY 1141 CAAATTTGGGATCTGGAAGATGATTTTGAAGTGTCTTCCAAACGACTTGGAAATGCTTACG 1200
 DB 1141 CAAATTTGGGATCTGGAAGATGATTTTGAAGTGTCTTCCAAACGACTTGGAAATGCTTACG 1200
 OY 1201 CAGAGCAGGATCTCTTAAATTTGGGAAACAAACAAATTCAGGGCTATCCAGCTGTATCA 1260
 DB 1201 CAGAGCAGGATCTCTTAAATTTGGGAAACAAACAAATTCAGGGCTATCCAGCTGTATCA 1260
 OY 1261 CAGTGTCTATGAACATATGATGATGTTGTGGAAGAAATTTATGATTCATGTTTAAATATCA 1320
 DB 1261 CAGTGTCTATGAACATATGATGATGTTGTGGAAGAAATTTATGATTCATGTTTAAATATCA 1320
 OY 1321 CCTCAGTGTGCGCCAGGTTGAGAGAGGATGCTTTGAGCTTACCAATTCATAGTCT 1380
 DB 1321 CCTCAGTGTGCGCCAGGTTGAGAGAGGATGCTTTGAGCTTACCAATTCATAGTCT 1380
 OY 1381 CCTTTTGAATGTCGAGATTAATGCTGATGTTTAAAGAAAGTATCTCAAAATCTCAAA 1440
 DB 1381 CCTTTTGAATGTCGAGATTAATGCTGATGTTTAAAGAAAGTATCTCAAAATCTCAAA 1440
 OY 1441 TATTTCTATGAACATCCACAGAAATGAAGACATACAGTTTATCATTTGATTCACCTTT 1500
 DB 1441 TATTTCTATGAACATCCACAGAAATGAAGACATACAGTTTATCATTTGATTCACCTTT 1500
 OY 1501 TTTCTGAGTAAAAATTTTACAGAAATTCCTTCCAAAGTTTACGAGAGACTCCAGGACTT 1560
 DB 1501 TTTCTGAGTAAAAATTTTACAGAAATTCCTTCCAAAGTTTACGAGAGACTCCAGGACTT 1560
 OY 1561 TGACAAAAGCAACCAATATTTGTTAAGATGATGAATCAATCAATGTTTTCGGAAG 1620
 DB 1561 TGACAAAAGCAACCAATATTTGTTAAGATGATGAATCAATCAATGTTTTCGGAAG 1620
 OY 1621 AGCATTTTATGATCCATTAAGGTTTACAGAGACCTTTTATTAAGGATGTCATATGTC 1680
 DB 1621 AGCATTTTATGATCCATTAAGGTTTACAGAGACCTTTTATTAAGGATGTCATATGTC 1680
 OY 1681 TCACAGAGCCACACAAAGTATGAGAGGAGTCAATTCACAGAAATTTATATGATGCTCTGTT 1740
 DB 1681 TCACAGAGCCACACAAAGTATGAGAGGAGTCAATTCACAGAAATTTATATGATGCTCTGTT 1740
 OY 1741 TGATATGAAGAAAGCAAAATGATGACCTTCCAGAGCCTGGGAGATGTGAAGAGACATTC 1800
 DB 1741 TGATATGAAGAAAGCAAAATGATGACCTTCCAGAGCCTGGGAGATGTGAAGAGACATTC 1800

Oy		1801	TGTTGCAGCCCTTCACAGCGCAGCGACGCTTGAGTGAAGTAGCTTAAGACA	1860
Db		1801	TGTTGCAGCCCTTCACAGCGCAGCGACGCTTGAGTGAAGTAGCTTAAGACA	1860
Oy		1861	TTCTTTAGAGACTGTATGTAATTGCTGTATGTCACCAAGAATAAATGGSTA	1920
Db		1861	TTCTTTAGAGACTGTATGTAATTGCTGTATGTCACCAAGAATAAATGGSTA	1920
Oy		1921	TATTCATPAATTTTTAAATTTGGTATPATTTGAATPAAGCTGAATATATATAAAAA	1960
Db		1921	TATTCATPAATTTTTAAATTTGGTATPATTTGAATPAAGCTGAATATATATAAAAA	1960
Oy		1981	AAAAAAAAAAAAA 1992	
Db		1981	AAAAAAAAAAAAA 1992	
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RESULT 2				
ID	AAO65520	standard; cDNA; 2653 BP.		
XX	AAO65520;			
XX				
DT	25-MAR-2003	(updated)		
DF	11-JAN-1995	(first entry)		
XX				
DE	Prostate-specific membrane antigen cDNA.			
XX				
KV	Prostate-specific membrane antigen; PSM; prostate cancer;			
KW	transmembrane glycoprotein; imaging; targeting; tumour detection;			
KX	antibody detection; ds.			
OS	Homo sapiens.			
FH	Key	Location/Qualifiers		
FT	CDS	262..2514		
FT		/*tag= a		
FT		/product= prostate specific membrane antigen (PSM)		
XX				
PN	WO9409820-A1.			
PD	11-MAY-1994.			
XX				
PF	05-NOV-1993;	93WO-US10624.		
PR	05-NOV-1992;	92US-0973337.		
XX				
PA	(SLOK) SLOAN KETTERING INST CANCER.			
XX				
PI	Fair WR, Heston MDW, Israeli RS;			
XX				
DR	WPI; 1994-167129/20.			
XX	P-PSDB; AAR55097.			
PT	Prostate-specific membrane antigen and DNA encoding it - is			
PT	useful for detecting haematogenous micro-metastatic tumour cells			
PT	and for identifying ligands which bind to PSM Ag			
XX				
XX	Claim 3; Page 103-106; 196pp; English.			
XX				
CC	AAO65520 encodes a prostate specific membrane antigen (PSM, AAR55097).			
CC	The PSM coding sequence is useful for suppressing or modulating the			
CC	metastatic ability of prostate tumour cells to grow, or for			
CC	eliminating them. The protein is useful to identify or purify ligands			
CC	of the Ag. It is also an attractive target for Ab-directed imaging			
CC	and targeting of prostatic tumour deposits.			
CC	(Updated on 25-MAR-2003 to correct PN field.)			
XX				
XQ	Sequence 2653 BP; 782 A; 524 C; 640 G; 707 T; 0 other:			
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Query Match	85.5%; Score 1702.6; DB 15; Length 2653;			
Best Local Similarity	98.5%; Pred. No. 0;			

	Matches	1729;	Conservative	0;	Mismatches	24;	Indels	2;	Gaps	1;
QY	240	AGGTTAAATATGCCAGCTGGCAGGGGCCAAAGAGTCAATTCCTACTCAGACCCCTGCTG	299							
Db	899	AGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGAGTCAATTCCTACTCAGACCCCTGCTG	958							
QY	300	ACTACTTTCGCTCGGGGGTGAAGTCCATACAGACGGTTGGAAATCTTCCTGAGAGTGGTG	359							
Db	959	ACTACTTTCGCTCGGGGGTGAAGTCCATACAGATGGTTGGAAATCTTCCTGAGAGTGGTG	1018							
QY	360	TCCAGCCGTGAATAATCCTTAATCTGAAATGGTGCAGAGACCCCTCTACACACAGATTACC	419							
Db	1019	TCCAGCCGTGAATAATCCTTAATCTGAAATGGTGCAGAGACCCCTCTACACACAGATTACC	1078							
QY	420	CAGCAATATGAATACGCTTATATGCGCATGGAATTGCAGAGCGTGTGGTCTTCCAAATATTC	479							
Db	1079	CAGCAATATGAATATGCTTATATGCGCGTGAATTCAGAGCGTGTGGTCTTCCAAATATTC	1138							
QY	480	CTGTTTCATCCAGTTGGATPACTATGATGCACAGAAAGCTCTGAAAAAAATGGGTGGCTCAG	539							
Db	1139	CTGTTTCATCCAAATTGGATPACTATGATGCACAGAAAGCTCTTGAAAAAATGGGTGGCTCAG	1198							
QY	540	CACCAACCATAGACAGCTGGAGAGAAAGTCTCAAAATGTCTCTACAAATGTTGGACCTGGCT	599							
Db	1199	CACCAACCCGATAGACAGCTGGAGAGAAAGTCTCAAAATGTCTCTACAAATGTTGGACCTGGCT	1258							
QY	600	TTACTGGAATCTTTTCTACAAAAAGTCAAGATGACATCCACTCTAACCAATGAATGA	659							
Db	1259	TTACTGGAATCTTTTCTACAAAAAGTCAAGATGACATCCACTCTAACCAATGAATGA	1318							
QY	660	CGAGAAATTTACAAATGTGATAGTACTCTCAAGAGACAGTGGAAACACAGACATATGTCA	719							
Db	1319	CAAGAAATTTACAAATGTGATAGTACTCTCAAGAGACAGTGGAAACACAGACATATGTCA	1378							
QY	720	TTCGCGGAGGTACCCGGGACTCATGGGTGTTTGGTATGACCCCTCAGAGTGGAGCAG	779							
Db	1379	TTCGCGGAGGTACCCGGGACTCATGGGTGTTTGGTATGACCCCTCAGAGTGGAGCAG	1438							
QY	780	CTGTTGTTTCATGAAGAACTGTGAGAGCTTTGGAACTGAAGAAAGAGGGGTGAGACCTA	839							
Db	1439	CTGTTGTTTCATGAAGAACTGTGAGAGCTTTGGAACTGAAGAAAGAGGGGTGAGACCTA	1498							
QY	840	GAAAGAACAAATTTGTTCGCAAGCTGGGATGCAGAGAAATTTGTGCTTCCTGTTCTACTG	899							
Db	1499	GAAAGAACAAATTTGTTCGCAAGCTGGGATGCAGAGAAATTTGTGCTTCCTGTTCTACTG	1558							
QY	900	AGTGGCAGAGATTAATCAAGACTCCCTCAAGAGCGGTGGCTTATTTAATCCTG	959							
Db	1559	AGTGGCAGAGATTAATCAAGACTCCCTCAAGAGCGGTGGCTTATTTAATCCTG	1618							
QY	960	ACTCATCTATATGAAGGAAACTACTCTGAGAGTTGATTTGTACACCACTGATGTACAGCT	1019							
Db	1619	ACTCATCTATATGAAGGAAACTACTCTGAGAGTTGATTTGTACACCACTGATGTACAGCT	1678							
QY	1020	TGGAATATCAACCTTAACAAAAGCGTGAAGAACCCCTGATGAAGCGTTTGAAGGCAAAATCTC	1079							
Db	1679	TGGAATATCAACCTTAACAAAAGCGTGAAGAACCCCTGATGAAGCGTTTGAAGGCAAAATCTC	1738							
QY	1080	TTTATATGAAGTTGGACTAAAAAAAGTCTTCGCCAGATTCAATGGGATGCCAGAGATTA	1139							
Db	1739	TTTATATGAAGTTGGACTAAAAAAAGTCTTCGCCAGATTCAATGGGATGCCAGAGATTA	1798							
QY	1140	GCAAAATTTGGATCTGGAAATGATTTTGAAGTGTTCCTTCCACGACCTTGGAAATTTGCTTCAG	1199							
Db	1799	GCAAAATTTGGATCTGGAAATGATTTTGAAGTGTTCCTTCCACGACCTTGGAAATTTGCTTCAG	1858							
QY	1200	GCAAGACACGGTATACTATAAAAATTGGGAAACAAACAAATTCAGGGCGTATCCATCTGATTC	1259							
Db	1859	GCAAGACACGGTATACTATAAAAATTGGGAAACAAACAAATTCAGGGCGTATCCATCTGATTC	1918							
QY	1260	ACAAGTCTCTATGAACAATATGATGGTGTGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1319							
Db	1919	ACAAGTCTCTATGAACAATATGATGGTGTGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1978							

QY	1320	ACCTCAGCTGCGCCAGGTTGCAGAGGAGTGGTTTGACTGTGCCAAATTCGATAGTC	1379
Db	1979	ACCTCAGCTGCGCCAGGTTGCAGAGGAGTGGTTTGACTGTGCCAAATTCGATAGTC	2038
QY	1380	TCCCTTTTGATTGTGAGATTATGCTGTAGTGTTTTAAAGAAATGATCTGACAAATCTTACA	1439
Db	2039	TCCCTTTTGATTGTGAGATTATGCTGTAGTGTTTTAAAGAAATGATCTGACAAATCTTACA	2098
QY	1440	ATATTTTCTATGAACATCCACAGAAATGAAGACATACAGTTTATCATTTGATTCACCTTT	1499
Db	2099	GTATTTCTATGAACATCCACAGAAATGAAGACATACAGTTTATCATTTGATTCACCTTT	2158
QY	1500	TTTTTCGAGTAAAAAATTTTACAGAAATTTGCTTCCAACTTGCAGCAGAGCTCCAGAGCT	1559
Db	2159	TTTTTCGAGTAAAAAATTTTACAGAAATTTGCTTCCAACTTGCAGCAGAGCTCCAGAGCT	2218
QY	1560	TTGACAAAAGACACCCCAATATTGTTAAGAAATGATGAATGATCAACTATGTTCTGAAA	1619
Db	2219	TTGACAAAAGACACCCCAATATTGTTAAGAAATGATGAATGATCAACTATGTTCTGAAA	2278
QY	1620	GAGCATTTATGATGCCATTAGGCTTACACAGAACACCTTTTATAGCATGTCTATGTG	1679
Db	2279	GAGCATTTATGATGCCATTAGGCTTACACAGAACACCTTTTATAGCATGTCTATGTG	2338
QY	1680	CTCCAGAGCAGCACAAACAATGTCAGAGGAGTCAATTTCCAGAAATTTATGATGCTCTGT	1739
Db	2339	CTCCAGAGCAGCACAAACAATGTCAGAGGAGTCAATTTCCAGAAATTTATGATGCTCTGT	2398
QY	1740	TTGATATTGAAGCAAAAGTGGACCCCTTCCAAAGCCCTGGGAGATGTGAAGACAGATTT	1799
Db	2399	TTGATATTGAAGCAAAAGTGGACCCCTTCCAAAGCCCTGGGAGATGTGAAGACAGATTT	2458
QY	1800	CTGTGTGACGCTTACAGTGCAGGACAGTGCAGAGACCTTGAAGAAATGATACCTTAAGAG	1859
Db	2459	ATGTTTGCAGCCTTACAGTGCAGGACAGTGCAGAGACCTTGAAGAAATGATACCTTAAGAG	2518
QY	1860	ATTCTTTTGAAGACCTCTGTATTGAAATTTGTGTATGTCACTC--AAAGATAATTAATAG	1917
Db	2519	ATTCTTTTGAAGAAATCCGATTTGAAATTTGTGTATGTCACTCAGAAAGAAATCGTAATG	2578
QY	1918	GTAATATTGATTAATTTTAAATTTGATATTTTGAAGAAAGTTGAATTTATATATATAAA	1977
Db	2579	GTAATATTGATTAATTTTAAATTTGATATTTTGAAGAAAGTTGAATTTATATATATAAA	2638
QY	1978	AAAAAAAAAAAAAAAAA 1992	
Db	2639	AAAAAAAAAAAAAAAAA 2653	
RESULT 3			
ABX03677 standard; DNA; 2653 BP.			
ID	ABX03677		
AC	ABX03677:		
DT	08-JAN-2003 (first entry)		
XX			
DE	DNA encoding folate hydrolase (prostate specific membrane antigen) 1.		
XX			
KW	Cell-mediated immunity; cellular immune response; CTL response;		
KW	tumour neovasculation; anti-angiogenesis; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200269907-A2.		
XX			
PD	12-SEP-2002.		
XX			
PF	07-MAR-2002; 2002WO-US07204.		
XX			
PR	07-MAR-2001; 2001US-274063P.		
XX			

PA	(CTLI-) CTL IMMUNOTHERAPIES CORP.
XX	
EI	Simard JUL, Diamond DC;
XX	
DR	WPI; 2002-750433/81.
XX	
DR	P-PSDB; ABG98045.
PT	Evaluating cell-mediated immunity, in particular cytotoxic T lymphocyte responses, by implanting vascular cells, useful for treatment and research models for directly targeting tumor neovasculature -
XX	
PS	Example 5; Page 28; 73pp; English.
XX	
CC	The invention describes a method of evaluating cell-mediated immunity comprising implanting vascular cells into an immunodeficient mammal,
CC	establishing an immune response in the mammal, and assaying a
CC	characteristic to determine cell-mediated immunity in the mammal. The
CC	methods and compositions of the present invention are useful for the
CC	generation of a cellular immune response, in particular a CTL response,
CC	for treatment directly against a tumour neovasculature. They can also be
CC	used for making research models targeting tumour neovasculature. The
CC	present invention using the anti-angiogenesis approach takes advantage
CC	of the need of tumors to recruit a blood supply to support their
CC	continued growth. This approach aims to disrupt a tumour's supply of
CC	nutrients to cause it to die or at least limit its growth. This sequence
CC	represents a DNA associated with the neo-vasculature preparation for
CC	treatment of cancer described in the invention.
XX	
S0	Sequence 2653 BP; 782 A; 524 C; 640 G; 707 T; 0 other;
	Query Match 85.5%; Score 1702.6; DB 24; Length 2653;
	Best Local Similarity 98.5%; Pred. No. 0;
	Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
OY	240 AGTTAAAGATGCCACTGGCAGGGCCCAAAGAGTCATTCTTACTACAGACCCTCGT 299
Dd	899 AGGTAAAAAATGCCCACTGGCAGGGCCCAAAGAGTCATTCTTACTCCGACCCTCGT 958
OY	300 ACTACTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTGGAAATCTTCTGGAGGTGGT 359
Dd	959 ACTACTTTGGCTCCGGGGTGAAGTCCTATCCAGATGGTTGGAAATCTTCCGGAGGTGGT 1018
OY	360 TCCAGCGGTGAATAATCCTAAATCGTAATGGTGAGAGAACCCCTCACACCGAGTTACC 419
Dd	1019 TTCAGCGGTGAATAATCCTAAATCGTAATGGTGAGAGAACCCCTCACACCGAGTTACC 1078
OY	420 CAGCAAAATGATACGCTTATAGGCATGGAATTCGAGAGCGGTGGTGGCTTCCAAGTATTC 479
Dd	1079 CAGCAAAATGATATGCTTATAGCGCTGGAATTCGAGAGCGGTGGTGGCTTCCAAGTATTC 1138
OY	480 CTGTTTCATCCAGTTGGATCTATGATGCACAGAAGCTCTTAGAAAATGGGTGGCTCAG 539
Dd	1139 CTGTTTCATCCAGTTGGATCTATGATGCACAGAAGCTCTTAGAAAATGGGTGGCTCAG 1198
OY	540 CACACACAGATAGAGCGTGGAGAGAGTCACAAGTGTCTTACAAATGTTGGACCTGGCT 599
Dd	1199 CACACACAGATAGAGCGTGGAGAGAGTCACAAGTGTCTTACAAATGTTGGACCTGGCT 1258
OY	600 TTACTGGAACCTTTCTACACAAAAGTCAAGATGCACATCCACTCTTACCAATGAAGTGA 659
Dd	1259 TTACTGGAACCTTTCTACACAAAAGTCAAGATGCACATCCACTCTTACCAATGAAGTGA 1318
OY	660 CGAATAATTTCAATGATAGTACTCTCGAGAGAGAGAGTGAACCGACAGATATGTCA 719
Dd	1319 CGAATAATTTCAATGATAGTACTCTCGAGAGAGAGAGTGAACCGACAGATATGTCA 1378
OY	720 TTTCGGAGAGTCACCGGAGCTCATGAGGTGTTTGGTGATATGACCCCTCAGAGTGGACAG 779
Dd	1379 TTTCGGAGAGTCACCGGAGCTCATGAGGTGTTTGGTGATATGACCCCTCAGAGTGGACAG 1438
OY	780 CTGTTGTTTCATGAATACTGTAGAGACTTTGGAGACACTGAAAAAGAAAGGTGGAGACTTA 839
Dd	1439 CTGTTGTTTCATGAATACTGTAGAGACTTTGGAGACACTGAAAAAGAAAGGTGGAGACTTA 1498


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QY      840 GAAGAACAAATTTGTTGCAAGCTGGGATGCAGAAATTTGCTCTCTGTTCTACTG 899
      1499 GAAGAACAAATTTGTTGCAAGCTGGGATGCAGAAATTTGCTCTCTGTTCTACTG 1558
QY      900 AGTGGCAGAGGATTAATCAAGACTCTCCAGAGCGGTGGCGTGTATATTAATGCTG 959
      1559 AGTGGCAGAGGATTAATCAAGACTCTCCAGAGCGGTGGCGTGTATATTAATGCTG 1618
QY      960 ACTCATCTATAGAGAACTACACTCTGAGATTTGTTATACACATGATATACAGCT 1019
      1619 ACTCATCTATAGAGAACTACACTCTGAGATTTGTTATACACATGATATACAGCT 1678
QY      1020 TGGTATACAACTAAACAAAGAGCTGAAAAGCCCTGATGAGGCTTTGAAAGCAATCTC 1079
      1679 TGGTATACAACTAAACAAAGAGCTGAAAAGCCCTGATGAGGCTTTGAAAGCAATCTC 1738
QY      1080 TTTATGAAAGTTGGACTAAAAAAAGTCCTCCAGAGTTCACTGGCATGCCAGATTA 1139
      1739 TTTATGAAAGTTGGACTAAAAAAAGTCCTCCAGAGTTCACTGGCATGCCAGATTA 1798
QY      1140 GCAAAATGGGATCTGAAATGATTTGAGGTGTTCTTCCAGACACTTGGAAATGCTTCA 1199
      1799 GCAAAATGGGATCTGAAATGATTTGAGGTGTTCTTCCAGACACTTGGAAATGCTTCA 1858
QY      1200 GCAGACGACGATTAATAAAAAATTTGGGAAACAAACAAATTCACGCGCTATCCACTGATC 1259
      1859 GCAGACGACGATTAATAAAAAATTTGGGAAACAAACAAATTCACGCGCTATCCACTGATC 1918
QY      1260 ACAGTGTCTATGAAACATATGAGTTGGTGGAAAGTTTATGATCCAAATGTTTAAATATC 1319
      1919 ACAGTGTCTATGAAACATATGAGTTGGTGGAAAGTTTATGATCCAAATGTTTAAATATC 1978
QY      1320 ACCCTACGTGGGCCCGGTTCCAGAGGAGTGGTGTGTTAGCTAGCCAAATTCATATGTCG 1379
      1979 ACCCTACGTGGGCCCGGTTCCAGAGGAGTGGTGTGTTAGCTAGCCAAATTCATATGTCG 2038
QY      1380 TCCCTTTGATTTGTCAGATTAATGCTGATTTAAGAAAGTGTGTCACAAATCTACA 1439
      2039 TCCCTTTGATTTGTCAGATTAATGCTGATTTAAGAAAGTGTGTCACAAATCTACA 2098
QY      1440 ATATTTCTATGAAACATCCACAGAAATGAGACATATCATATTTGATTCATCTT 1499
      2099 ATATTTCTATGAAACATCCACAGAAATGAGACATATCATATTTGATTCATCTT 2158
QY      1500 TTTCTGCACTAAAAATTTTACAGAAATGCTTCCAGTTCCAGCCGAGACCTCCAGACT 1559
      2159 TTTCTGCACTAAAAATTTTACAGAAATGCTTCCAGTTCCAGCCGAGACCTCCAGACT 2218
QY      1560 TTGACAAAAGCAACCAATATTTGTTAAGATGATGAATGATCAATCATGTTCTGGAAA 1619
      2219 TTGACAAAAGCAACCAATATTTGTTAAGATGATGAATGATCAATCATGTTCTGGAAA 2278
QY      1620 GAGCATTTATGATTCATTAGGGTTACAGACAGACCTTTTATAGCATGTCATATATG 1679
      2279 GAGCATTTATGATTCATTAGGGTTACAGACAGACCTTTTATAGCATGTCATATATG 2338
QY      1680 CTCACAGCAGCCACAAACAGTATGCGGGGAGTGCATTTCCAGGAATTTATGATGCTCTGT 1739
      2339 CTCACAGCAGCCACAAACAGTATGCGGGGAGTGCATTTCCAGGAATTTATGATGCTCTGT 2398
QY      1740 TTGATTTGAAAGCAAAAGTGACCTTCCAGGCGCTGGGAGATGGAAGAGACATATTT 1799
      2399 TTGATTTGAAAGCAAAAGTGACCTTCCAGGCGCTGGGAGATGGAAGAGACATATTT 2458
QY      1800 CTGTGTCAGCTTACAGTGCAGGACGTCGAGAGACTTTGAGTGAAGTACCTTAAGAG 1859
      2459 CTGTGTCAGCTTACAGTGCAGGACGTCGAGAGACTTTGAGTGAAGTACCTTAAGAG 2518
QY      1860 ATTCTTTAGAGACTGTATTAATTTGTTGTTATGTCATGTCAC - -AAAATAATTAATG 1917
      2519 ATTCTTTAGAGACTGTATTAATTTGTTGTTATGTCATGTCACAAAAGAAATCTGAATG 2578

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QY      1918 GTATATTGATTAATTTTAAATTTGATATATTGAATTAAGTGAATATATATATATAA 1977
      2579 GTATATTGATTAATTTTAAATTTGATATATTGAATTAAGTGAATATATATATATAA 2638
QY      1978 AAAAAAAAAAAAAA 1992
      2639 AAAAAAAAAAAAAA 2653
Db
RESULT 4
ABK86204
ID      ABK86204 standard; cdna; 2653 BP.
XX
AC      ABK86204;
XX
DT      24-SEP-2002 (first entry)
XX
DE      cdna encoding human prostate specific membrane antigen (PSMA) variant.
XX
KW      Human; prostate specific membrane antigen; PSMA; cytostatic; antiviral;
KW      immunostimulant; cell-mediated immune response; tumour; breast cancer;
KW      virus infection; prostate cancer; colorectal cancer; pancreatic cancer;
KW      lymphoma; leukemia; hepatitis; lentivirus; herpesvirus;
KW      human immunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.
XX
OS      Homo sapiens.
XX
FH      key
FT      CDS
FT      262..2514
FT      /*tag= a
FT      /product= "Prostate specific membrane antigen (PSMA)
FT      variant with signal sequence deleted"
XX
PN      WO200240059-A2.
XX
PD      23-MAY-2002.
XX
PF      01-NOV-2001; 2001MO-US45626.
XX
PR      01-NOV-2000; 2000US-0704232.
XX
PA      (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.
PA      (MNC/) MINCHEFF M S.
PA      (LOUK/) LOUKINOV D I.
PA      (ZOUB/) ZOUBAK S.
XX
PI      Mincheff MS, Loukinov DI, Zoubak S;
XX
WPI: 2002-527524/56.
XX
P-PSDB: AAU98920.
XX
PT      Inducing a cell-mediated immune response against a target antigen,
PT      reducing undesired cells and stimulating presentation of an antigen by
PT      a cell, comprises administering a polynucleotide encoding a variant of
PT      an antigen -
XX
PS      Example 1; Page 114-118; 146pp; English.
XX
XX      The invention relates to a method of inducing a cell-mediated immune
XX      response against a cell comprising a target antigen (I) in a subject,
XX      treating a subject having undesired cells, for example tumour cells,
XX      or virally infected cells (C), reducing the number of (C) in a subject,
XX      and stimulating presentation of (I) by a cell. This is done by
XX      administering a polynucleotide (II) encoding a variant of (I), so that
XX      (II) expressed in a cell and cell-mediated immune response is induced.
XX      The method can be used to treat prostate cancer, breast cancer,
XX      colorectal cancer and pancreatic cancer, as well as lymphomas and
XX      leukemias. The method is also useful in treating chronic viral
XX      infections such as those caused by hepatitisviruses, lentiviruses
XX      (including human immunodeficiency virus (HIV)), herpesviruses and the
XX      flaviviruses and pestiviruses. The present sequence represents the coding
XX      sequence of human prostate specific membrane antigen (PSMA) variant
XX      which has the signal sequence deleted, used as a target antigen in the

```

CC method of the invention.

XX Sequence 2653 BP; 782 A; 524 C; 640 G; 707 T; 0 other;

Query Match 85.5% Score 1702.6; DB 24; Length 2653;

Best Local Similarity 98.5% Pred. No. 0; Mismatches 24; Indels 2; Gaps 1;

Matches 1729; Conservative 0;

240 AGGTTAAATGCGCCAGTGGCGGCAAGAGTCAATCTCTACTCAGACCCTGCTG 299
|||||
899 AGGTTAAATGCGCCAGTGGCGGCAAGAGTCAATCTCTACTCAGACCCTGCTG 958
|||||
300 ACTACTTTCCTCCGGGGTGAAGTCTTATCCAGACGGTGGATCTTCTGGAGTGGTG 359
|||||
959 ACTACTTTCCTCCGGGGTGAAGTCTTATCCAGATGGTGGAAATCTTCTGGAGTGGTG 1018
|||||
360 TCCAGCGGGGAAATATCTTAAATGATGATGGTGGAGAGACCTCTCAGACAGGTTACC 419
|||||
1019 TCCAGCGGGGAAATATCTTAAATGATGATGGTGGAGAGACCTCTCAGACAGGTTACC 1078
|||||
420 CAGCAAAATGATACGCTTATAGGCATGGAATTCAGAGGCTGTTGGTCTTCCAAAGTATTC 479
|||||
1079 CAGCAAAATGATACGCTTATAGGCATGGAATTCAGAGGCTGTTGGTCTTCCAAAGTATTC 1138
|||||
480 CTGTTTCATCCAGTTGGATCTATATGACACAGAACTCTTGAAAAAATGGGTGGCTCAG 539
|||||
1139 CTGTTTCATCCAGTTGGATCTATGATGACACAGAACTCTTGAAAAAATGGGTGGCTCAG 1198
|||||
540 CAGCACAAGATAGAGCTGGAGAGAGTGTCAAGTGTCTCAAAATGGTGGACCTGGCT 599
|||||
1199 CAGCACAAGATAGAGCTGGAGAGAGTGTCTCAAAATGGTGGACCTGGCT 1258
|||||
600 TTACTGGAACCTTTCTACACAAAAAGTCAAGATGACATCCACTCTACCAATGAATGA 659
|||||
1259 TTACTGGAACCTTTCTACACAAAAAGTCAAGATGACATCCACTCTACCAATGAATGA 1318
|||||
660 CGAGAAATTTACAAATGTATAGTACTCTCAGAGAGAGCGATGGAACACAGACAGATATGCA 719
|||||
1319 CAGAAATTTACAAATGTATAGTACTCTCAGAGAGAGCGATGGAACACAGACAGATATGCA 1378
|||||
720 TTCTGGAGGTCACCGGGACTCATAGGGGTTTGGTGATGTTGACCCCTCAGAGTGGAGAG 779
|||||
1379 TTCTGGAGGTCACCGGGACTCATAGGGGTTTGGTGATGTTGACCCCTCAGAGTGGAGAG 1438
|||||
780 CTGTTGTTTCATGAATCTGTGAGAGCTTTGGAAACATGAAAAAGGAGGTTGAGACCTTA 839
|||||
1439 CTGTTGTTTCATGAATCTGTGAGAGCTTTGGAAACATGAAAAAGGAGGTTGAGACCTTA 1498
|||||
840 GAAAGACAAATTTTGTGGCAAGCTGGGATGCAAGAAATTTGGTCTTCTGGTCTTACTG 899
|||||
1499 GAAAGACAAATTTTGTGGCAAGCTGGGATGCAAGAAATTTGGTCTTCTGGTCTTACTG 1558
|||||
900 AGTGGGCGAGAGATATCTCAAGACTCTTCAAGAGCGTGGGCTTATATTATGCTG 959
|||||
1559 AGTGGGCGAGAGATATCTCAAGACTCTTCAAGAGCGTGGGCTTATATTATGCTG 1618
|||||
960 ACTCATCTATAGAAAGAACTACACTGTGAGAGTTGATTTGACACCACTGATGTACAGCT 1019
|||||
1619 ACTCATCTATAGAAAGAACTACACTGTGAGAGTTGATTTGACACCACTGATGTACAGCT 1678
|||||
1020 TGGTATACACCTTAACAAAGAGCTGAAAAGCCCTGATGAGAGGCTTTTAAAGCAAAATCTC 1079
|||||
1679 TGGTATACACCTTAACAAAGAGCTGAAAAGCCCTGATGAGAGGCTTTTAAAGCAAAATCTC 1738
|||||
1080 TTTATGAAGTTGGACTAAAAAAGTCCCTCCCGAGTTCAGTGGCAGTCCAGAGATTA 1139
|||||
1739 TTTATGAAGTTGGACTAAAAAAGTCCCTCCCGAGTTCAGTGGCAGTCCAGAGATTA 1798
|||||
1140 GCAAAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCAAAGCAAGCTTGAATGGCTTCA 1199
|||||
1799 GCAAAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCAAAGCAAGCTTGAATGGCTTCA 1858
|||||
1200 GCAGAGCAGGTAATCTAAAAAATTTGGAAACAAACAAATTTACGGGCTATCTCAGCTGTATC 1259

|||||
1859 GCAGAGCAGGTAATCTAAAAAATTTGGAAACAAACAAATTTACGGGCTATCTCAGCTGTATC 1918
|||||
1260 ACAAGTCTATGAAACATATGAGTGGTGGAAAAAGTTTATGATGCCAATCTTTAAATATC 1319
|||||
1919 ACAAGTCTATGAAACATATGAGTGGTGGAAAAAGTTTATGATGCCAATCTTTAAATATC 1978
|||||
1320 ACCTCACATGGGCCCGAGGTCGAGAGAGGATGGTGGTGGGTCGATGCCAATTCATATGTC 1379
|||||
1979 ACCTCACATGGGCCCGAGGTCGAGAGAGGATGGTGGTGGGTCGATGCCAATTCATATGTC 2038
|||||
1380 TCCCTTTGATGTCAGATTTATGCTGATTTTAAAGATATGCTGACAAAAATCTACA 1439
|||||
2039 TCCCTTTGATGTCAGATTTATGCTGATTTTAAAGATATGCTGACAAAAATCTACA 2098
|||||
1440 ATATTTCTATGAACATCCACAGAAATGGAACATACAGTTATCATTTGATTCCTTT 1499
|||||
2099 GTATTTCTATGAACATCCACAGAAATGGAACATACAGTTATCATTTGATTCCTTT 2158
|||||
1500 TTTCTGCAATGAAAAATTTTACAGAAATTTGCTCCCAAGTTCCAGGAGAGACTCCAGACT 1559
|||||
2159 TTTCTGCAATGAAAAATTTTACAGAAATTTGCTCCCAAGTTCCAGGAGAGACTCCAGACT 2218
|||||
1560 TTGACAAAGCAACCCCAATATTTGTAAGATGATGATGATCAACTCATGTTTCTGAAA 1619
|||||
2219 TTGACAAAGCAACCCCAATATTTAAGATGATGATGATGATCAACTCATGTTTCTGAAA 2278
|||||
1620 GAGCATTTATTTGATTCATTAAGGTTTACACAGACACTTTTATAGCATGTCATCTATG 1679
|||||
2279 GAGCATTTATTTGATTCATTAAGGTTTACACAGACACTTTTATAGCATGTCATCTATG 2338
|||||
1680 CTCACAGCAGCACAACAAAGTATGACAGGAGGATGTCACAGAAATTTATGATGCTGT 1739
|||||
2339 CTCACAGCAGCACAACAAAGTATGACAGGAGGATGTCACAGAAATTTATGATGCTGT 2398
|||||
1740 TTGATTTTGAAGCAAGTGGACCTTCCAAAGGCTGGGAGATGTAAGAGACAGATTT 1799
|||||
2399 TTGATTTTGAAGCAAGTGGACCTTCCAAAGGCTGGGAGATGTAAGAGACAGATTT 2458
|||||
1800 CTGTTGACGCTTTCACAGTGGAGCAGCTGACAGACTTTGATGAAAGTACCTTAAGAG 1859
|||||
2459 ATGTTGACGCTTTCACAGTGGAGCAGCTGACAGACTTTGATGAAAGTACCTTAAGAG 2518
|||||
1860 ATTCCTTAAGACCTGATGATGATTTGTGGTATGTCACCTC--AAAGATAATTAATG 1917
|||||
2519 ATTCCTTAAGACCTGATGATGATTTGTGGTATGTCACCTC--AAAGATAATTAATG 2578
|||||
1918 GTATATGATTAATTTTAAATTTGATATTTGAAATTAAGTTGAATTAATTAATAA 1977
|||||
2579 GTATATGATTAATTTTAAATTTGATATTTGAAATTAAGTTGAATTAATTAATAA 2638
|||||
1978 AAAAAAAAAAAAAA 1992
|||||
2639 AAAAAAAAAAAAAA 2653
|||||
RESULT 5
ABK64556
ID ABK64556 standard; DNA: 2653 BP.
XX
AC ABK64556;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human benign prostatic hyperplasia gene #451.
KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
OS Homo sapiens.
XX
PN WO200212440-A2.
XX
PD 14-FEB-2002.

DB 2339 CTCACAGCAGCCACACAGTATGACGGGAGTCATTCCAGAAATTTATGATGCTCTGT 2398
OY 1740 TTGATATTTGAAGCAAGTGGACCTTCCAAAGCCTGGGAGATGTAAGAGACAGATTT 1799
DB 2399 TTATATTTGAAGCAAGTGGACCTTCCAAAGCCTGGGAGATGTAAGAGACAGATTT 2458
OY 1800 CTGTTCAGCCTTCACAGTGCAGCAGCTCAGAGACTTGTAGTGAAGTAAAGG 1859
DB 2459 ATGTTCAGCCTTCACAGTGCAGCAGCTCAGAGACTTGTAGTGAAGTAAAGG 2518
OY 1860 ATTCTTTAGAGACTGTATATGTAATTTGTGTGTCTACTC--AAAGATATATATGG 1917
DB 2519 ATTCTTTAGAGAAATCCGATATGTAATTTGTGTGTCTACTCAGAAAGATCGTAATGG 2578
OY 1918 GTATATGATAAATTTTAAATTTGATATTTGAAATGAATATATATATATAA 1977
DB 2579 GTATATGATAAATTTTAAATTTGATATTTGAAATGAATATATATATATAA 2638
OY 1978 AAAAAAAAAAAAAA 1992
DB 2639 AAAAAAAAAAAAAA 2653
RESULT 6
ABL69670 ID ABL69670 standard; DNA: 2653 BP.
XX ABL69670:
AC
XX
DT 15-MAY-2002 (first entry)
DE
XX
XX Prostate cancer related gene sequence SEQ ID NO:8007.
XX
KM Human: cancer: colon; breast; ovary; oesophagus; kidney; thyroid;
KM stomach; lung; prostate; pancreas; carcinoma; antitumor; cancerous;
KM cytoskeletal; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
KM gene; ds.
XX
OS Homo sapiens.
XX
PN W0200194629-A2.
PD
XX 13-DEC-2001.
XX
PF 30-MAY-2001; 2001MO-US10838.
XX
PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-231133P.
PR 18-SEP-2000; 2000US-231617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234505P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.

PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
XX (AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Sopfel DR, Weaver Z;
XX
XX WPI: 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set
XX
PS Claim 1; SEQ ID 8007; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytoskeletal
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.
XX
SQ Sequence 2653 BP; 782 A; 524 C; 640 G; 707 T; 0 other;
Query Match 85.5%; Score 1702.6; DB 24; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
OY 240 AGGTTAAATGCCCAGCTGGCAGGGGCCAAAGAGTCATCTCTACTGAGCCCTGCG 299
DB 899 AGGTTAAATGCCCAGCTGGCAGGGGCCAAAGAGTCATCTCTACTGAGCCCTGCG 958
OY 300 ACTACTTGTGCTCGGGGGTGAAGTCCATTCAGACGGTGGAAATCTTCGAGGTGGTG 359
DB 959 ACTACTTGTGCTCGGGGGTGAAGTCCATTCAGATGTTGGAAATCTTCGAGGTGGTG 1018
OY 360 TCCAGCGTGAATATCTTAATCTGAATGGTGCAGAGACCTCTCACACAGGTTACC 419
DB 1019 TCCAGCGTGAATATCTTAATCTGAATGGTGCAGAGACCTCTCACACAGGTTACC 1078
OY 420 CAGCAATGAATACGCTTATAGCATGGAATTCAGAGGCTGTGGCTCCCAAGATTC 479
DB 1079 CAGCAATGAATATGCTTATAGCGTGAATTCAGAGGCTGTGGCTCCCAAGATTC 1138
OY 480 CTGTTCAATCCAGTTGATATGATGCACAGAGCTCTAGAAAAAATGGTGGCTAC 539
DB 1139 CTGTTCAATCCAGTTGATATGATGCACAGAGCTCTAGAAAAAATGGTGGCTAC 1198

QY 540 CACCACAGATAGCAGCTGGAGGAGAGTCTCAAAAGTCCATGTTGACCGGCT 599
 |||||
 Db 1199 CACACACAGATAGCAGCTGGAGGAGAGTCTCAAAAGTCCATGTTGACCGGCT 1258
 QY 600 TTACTGGAAACCTTTCTACACAAAAGTCACATCCACTCCACCAATGAAGTGA 659
 |||||
 Db 1259 TTACTGGAAACCTTTCTACACAAAAGTCACATCCACTCCACCAATGAAGTGA 1318
 QY 660 CGGAATTTACATGATGATGATCTCTAGAGACAGTGAACAGACAGATATGCTA 719
 |||||
 Db 1319 CAGGAATTTACATGATGATGATCTCTAGAGACAGTGAACAGACAGATATGCTA 1378
 QY 720 TTCTGGAGAGTACCGGAGCTCATGGGTGTTGGTATTTGACCTTCAGAGTGAAG 779
 |||||
 Db 1379 TTCTGGAGAGTACCGGAGCTCATGGGTGTTGGTATTTGACCTTCAGAGTGAAG 1438
 QY 780 CTCTTTTCATGAACCTGTGAGAGAGCTTTGGAACCTGAAGAAAGAGGTGAGACTA 839
 |||||
 Db 1439 CTCTTTTCATGAACCTGTGAGAGAGCTTTGGAACCTGAAGAAAGAGGTGAGACTA 1498
 QY 840 GAAGAACAAATTTGTTGCAAGCTGGATGCAAGAAATTTGCTCTTGGTCTACAG 899
 |||||
 Db 1499 GAAGAACAAATTTGTTGCAAGCTGGATGCAAGAAATTTGCTCTTGGTCTACAG 1558
 QY 900 AGTGGCAGAGATTAATTAAGACTCTTCAAGAGCGTGGCGCTTATTAATGCTG 959
 |||||
 Db 1559 AGTGGCAGAGATTAATTAAGACTCTTCAAGAGCGTGGCGCTTATTAATGCTG 1618
 QY 960 ACTCATCTATAGAGGAAACCTACCTGTAGAGTGTATGTACACCATGATGTACAGCT 1019
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 Db 1619 ACTCATCTATAGAGGAAACCTACCTGTAGAGTGTATGTACACCATGATGTACAGCT 1678
 QY 1020 TGGTATACCAACCTAACAAAGAGCTGAAGAGCTTATGAAGCTTTGAAGGAAATCTC 1079
 |||||
 Db 1679 TGGTATACCAACCTAACAAAGAGCTGAAGAGCTTATGAAGGAAATCTC 1738
 QY 1080 TTTATGAAAGTGGACTAAAAAGTCTTCCACAGTTCAGTGGCATGCCAGATTA 1139
 |||||
 Db 1739 TTTATGAAAGTGGACTAAAAAGTCTTCCACAGTTCAGTGGCATGCCAGATTA 1798
 QY 1140 GCAAAATTTGGGATCTGAAAAATGATTTGAGGTGTTCTTCCACAGACTTGAATTTGCTCAG 1199
 |||||
 Db 1799 GCAAAATTTGGGATCTGAAAAATGATTTGAGGTGTTCTTCCACAGACTTGAATTTGCTCAG 1858
 QY 1200 GGAGAGCAGGATTAATAAATTTGGGAAACAAACAAATTCAGCGGCTATCCACTGATC 1259
 |||||
 Db 1859 GGAGAGCAGGATTAATAAATTTGGGAAACAAACAAATTCAGCGGCTATCCACTGATC 1918
 QY 1260 ACAGTGTCTATGAACATATGATGTTGGAAAAAGTTTTATGATCCAAATGTTAAATATC 1319
 |||||
 Db 1919 ACAGTGTCTATGAACATATGATGTTGGAAAAAGTTTTATGATCCAAATGTTAAATATC 1978
 QY 1320 ACCTCACGTGTGGCCAGGTTCGAGAGGAGGTGTTGAGCTAGGCCAAATCCCATAGTGC 1379
 |||||
 Db 1979 ACCTCACGTGTGGCCAGGTTCGAGAGGAGGTGTTGAGCTAGGCCAAATCCCATAGTGC 2038
 QY 1380 TCCCTTTGATGTGAGATTAATGCTGTGTTTAAGAAAGTATGCTGACAAATCTTACA 1439
 |||||
 Db 2039 TCCCTTTGATGTGAGATTAATGCTGTGTTTAAGAAAGTATGCTGACAAATCTTACA 2098
 QY 1440 AATATTTCTATGAACATCCACAGGAATGAGACATACAGTTATCATTTGATTCCTTT 1499
 |||||
 Db 2099 GATATTTCTATGAACATCCACAGGAATGAGACATACAGTTATCATTTGATTCCTTT 2158
 QY 1500 TTTCTGACGTAAAAATTTTACAGAAATTTCTCAAGTTCAAGCGAGAGACTCCAGGACT 1559
 |||||
 Db 2159 TTTCTGACGTAAAAATTTTACAGAAATTTCTCAAGTTCAAGCGAGAGACTCCAGGACT 2218
 QY 1560 TTGACAAAAGCAACCAATATTTGTTAAGATGATGATGATCAACCTCATGTTCTGGAAA 1619
 |||||
 Db 2219 TTGACAAAAGCAACCAATATTTGTTAAGATGATGATGATCAACCTCATGTTCTGGAAA 2278

QY 1620 GAGCATTTATGATTCATTAGGGTTACAGACAGACCTTTTATAGCATGTCATATG 1679
 |||||
 Db 2279 GAGCATTTATGATTCATTAGGGTTACAGACAGACGCTTTTATAGCATGTCATATG 2338
 QY 1680 CTCGAAGCAGCCACAACAAGTATGAGGGGAGTCAATCCAGGAATTTATGATGCTGCT 1739
 |||||
 Db 2339 CTCGAAGCAGCCACAACAAGTATGAGGGGAGTCAATCCAGGAATTTATGATGCTGCT 2398
 QY 1740 TTGATATTGAAGCAAGTGGAGCCCTTCCAGGCCCTGGGAGCATGTGAAGACACATTT 1799
 |||||
 Db 2399 TTGATATTGAAGCAAGTGGAGCCCTTCCAGGCCCTGGGAGCATGTGAAGACACATTT 2458
 QY 1800 CTGTTGACAGCTTTCACAGTGCAGAGCGAGCTGCAGAGACTTTGAGTGAAGTAAAGAG 1859
 |||||
 Db 2459 ATGTTGACAGCTTTCACAGTGCAGAGCGAGCTGCAGAGACTTTGAGTGAAGTAAAGAG 2518
 QY 1860 ATTCTTTAGAGACTCTGTAATTTGATTTGTGTGATGTCACCTC --AAAGATTAATATG 1917
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 Db 2519 ATTCTTTAGAGACTCTGTAATTTGATTTGTGTGATGTCACCTCAGAAAGATCGTAATGG 2578
 QY 1918 GTATATTGAATTAATTTTAAATTTGATATTGTAATTAAGTGAATTTATATATATAA 1977
 |||||
 Db 2579 GTATATTGAATTAATTTTAAATTTGATATTGTAATTAAGTGAATTTATATATATAA 2638
 QY 1978 AAAAAAAAAAAAAA 1992
 |||||
 Db 2639 AAAAAAAAAAAAAA 2653

RESULT 7
 AB083845
 ID AB083845 standard; cDNA; 2653 BP.
 XX
 AC AB083845;
 XX
 DT 03-FEB-2003 (first entry)
 XX
 DE Human P5MA encoding cDNA SEQ ID NO:7.
 XX
 KW Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
 KW T cell; enzyme; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WC0200281646-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 04-APR-2002; 2002WC-US11101.
 XX
 PR 06-APR-2001; 2001US-282211P.
 PR 07-NOV-2001; 2001US-337017P.
 PR 07-MAR-2002; 2002US-363210P.
 XX
 PA (CTL-) CTL IMMUNOTHERAPIES CORP.
 PI Simard JTL, Diamond DC, Liu L, Xie Z;
 XX
 DR WPI; 2003-067518/06.
 DR P-PSDB; ABP74131.
 XX
 PT Novel epitopes useful as vaccines, comprises peptides or nucleic acid
 PT encoding the peptides, that are useful epitopes of target-associated
 PT antigens -
 PS
 PS Claim 1; Page 149-151; 352pp; English.
 CC
 CC The present invention describes an isolated epitope (I) and an epitope
 CC cluster. Also described is a vaccine or immunotherapeutic composition
 CC (VC) comprising (I). (I) has cytostatic activity. VC is useful for
 CC treating an animal, by administering to an animal the vaccine or
 CC immunotherapeutic composition. VC is also useful for evaluating
 CC immunogenicity of a vaccine or immunotherapeutic composition, by

CC administering VC to an HLA-transgenic animal and evaluating
CC immunogenicity based on a characteristic of the animal, or by in vitro
CC primary stimulation of a T cell and evaluating immunogenicity. (1) is
CC useful for determining specific T cell frequency, by contacting T cells
CC with a MHC-peptide complex, and further comprises ELISPOT analysis,
CC limiting dilution analysis, flow cytometry, in situ hybridisation and/or
CC polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to
CC ABP74173 represent sequences used in the exemplification of the present
XX invention.

SO Sequence 2653 BP: 782 A; 524 C; 640 G; 707 T; 0 other:

Query Match 85.5%; Score 1702.6; DB 25; Length 2653;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

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OY 240 AGGTAAATATGCGCCAGCTGGCAGGGCCAAAGAGCATCTCTACTCAGACCCTGCTG 299
DB 899 AGGTAAATATGCGCCAGCTGGCAGGGCCAAAGAGCATCTCTACTCAGACCCTGCTG 958
OY 300 ACTACTTGGCTCCTGGGGTGAAGTCTATCCAGACGGTTGGAAATCTTCTGGAGTGGTG 359
DB 959 ACTACTTGGCTCCTGGGGTGAAGTCTATCCAGATGGTTGGAATCTTCTGGAGTGGTG 1018
OY 360 TCCAGCGTGAATATCTCTAAATCTGAATGTCAGAGACCCCTCTACACAGGTTACC 419
DB 1019 TCCAGCGTGAATATCTCTAAATCTGAATGTCAGAGACCCCTCTACACAGGTTACC 1078
OY 420 CAGAAATGATATAGCTTATAGCATGATGATGATGATGATGATGATGATGATGATGATG 479
DB 1079 CAGAAATGATATAGCTTATAGCATGATGATGATGATGATGATGATGATGATGATGATG 1138
OY 480 CTGTTTATCCAGTTGATATCTATGATGATGATGATGATGATGATGATGATGATGATG 539
DB 1139 CTGTTTATCCAGTTGATATCTATGATGATGATGATGATGATGATGATGATGATGATG 1198
OY 540 CACCAACAGATAGACGCTGGAGAGAGATCTCAAAAGTCTCTACATTTGGAGCTGGCT 599
DB 1199 CACCAACAGATAGACGCTGGAGAGAGATCTCAAAAGTCTCTACATTTGGAGCTGGCT 1258
OY 600 TTACGGAACTTTTCTACACAAAAGTCAAGATGATGATGATGATGATGATGATGATGATG 659
DB 1259 TTACGGAACTTTTCTACACAAAAGTCAAGATGATGATGATGATGATGATGATGATGATG 1318
OY 660 CGAATATTTACAAATGTAGTACTCTCAGAGAGACGATGGAACACAGACATATGTCA 719
DB 1319 CGAATATTTACAAATGTAGTACTCTCAGAGAGACGATGGAACACAGACATATGTCA 1378
OY 720 TTCTGGAGGTCACCGGACATCATGGTGTGGTGTGATGATGATGATGATGATGATGATG 779
DB 1379 TTCTGGAGGTCACCGGACATCATGGTGTGGTGTGATGATGATGATGATGATGATGATG 1438
OY 780 CTGTTGTTTCAATGAATCTGAGAGCTTTGGAACCTGAAAAAGAGAGGAGACCTCA 839
DB 1439 CTGTTGTTTCAATGAATCTGAGAGCTTTGGAACCTGAAAAAGAGAGGAGACCTCA 1498
OY 840 GAAGAACTATTTTGTTCGAAGCTGGAGTGAAGAAATTTGGTCTTGGTTCTACTG 899
DB 1499 GAAGAACTATTTTGTTCGAAGCTGGAGTGAAGAAATTTGGTCTTGGTTCTACTG 1558
OY 900 AGTGGGACAGAGATATTCAGAGCTCTTCAAGACGCTGGCTGTATATATATGCTG 959
DB 1559 AGTGGGACAGAGATATTCAGAGCTCTTCAAGACGCTGGCTGTATATATATGCTG 1618
OY 960 ACTCATATGAAAGAACTACACTGAGAGTGTGATGATGATGATGATGATGATGATGATG 1019
DB 1619 ACTCATATGAAAGAACTACACTGAGAGTGTGATGATGATGATGATGATGATGATGATG 1678
OY 1020 TGGTATACACTAACAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGCAATCTC 1079
DB 1679 TGGTATACACTAACAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGCAATCTC 1738
OY 1080 TTTATGAAAGTTGCACTAAAAAAGTCTCTCCCGAGAGTTGATGAGCATGCCAGATTA 1139
```

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DB 1739 TTTATGAAAGTTGCACTAAAAAAGTCTCTCCCGAGAGTTGATGAGCATGCCAGATTA 1798
OY 1140 GCAATATGGGATCTGAAATGATTTGAGGTGTCTTCCAGACATCTTGAATGCTTCAAG 1199
DB 1799 GCAATATGGGATCTGAAATGATTTGAGGTGTCTTCCAGACATCTTGAATGCTTCAAG 1858
OY 1200 GCAGAGCAGGATATCTAATAAATTTGGAACAACAATTCAGCGCTATTCACGTATTC 1259
DB 1859 GCAGAGCAGGATATCTAATAAATTTGGAACAACAATTCAGCGCTATTCACGTATTC 1918
OY 1260 ACAGTGTCTATGAAACATATGAGTGTGGGAAAGTTTATGATGATGATGATGATGATG 1319
DB 1919 ACAGTGTCTATGAAACATATGAGTGTGGGAAAGTTTATGATGATGATGATGATGATG 1978
OY 1320 ACCTCATGTGGCCAGAGTTGAGAGAGAGATGATGATGATGATGATGATGATGATGATG 1379
DB 1979 ACCTCATGTGGCCAGAGTTGAGAGAGAGATGATGATGATGATGATGATGATGATGATG 2038
OY 1380 TCCCTTTGATTTGCGAGATTTATCTGATTTTAAAGAAATATGCTGACAAAATCTACA 1439
DB 2039 TCCCTTTGATTTGCGAGATTTATCTGATTTTAAAGAAATATGCTGACAAAATCTACA 2098
OY 1440 ATATTTCTATGAAACATCCACAGGAATGGAAGACATACATGATTTATGATTTCACTT 1499
DB 2099 ATATTTCTATGAAACATCCACAGGAATGGAAGACATACATGATTTATGATTTCACTT 2158
OY 1500 TTTCTGCGAGTAAAAATTTTACAGAAATTTGCTTCAAGTTTCAGGAGAGATCCAGAGCT 1559
DB 2159 TTTCTGCGAGTAAAAATTTTACAGAAATTTGCTTCAAGTTTCAGGAGAGATCCAGAGCT 2218
OY 1560 TTGCAAAAAGCAACCCATATTTGTAAGAAATGATGATGATGATGATGATGATGATGATG 1619
DB 2219 TTGCAAAAAGCAACCCATATTTGTAAGAAATGATGATGATGATGATGATGATGATGATG 2278
OY 1620 GAGCATTTATGATCCATTTAGGTTTACACAGACACCTTTTATAGCATCTCATATG 1679
DB 2279 GAGCATTTATGATCCATTTAGGTTTACACAGACACCTTTTATAGCATCTCATATG 2338
OY 1680 CTCCAGAGCAGCACACAAAGTATGAGGAGATCTTCCAGAAATTTATGATGCTCTGT 1739
DB 2339 CTCCAGAGCAGCACACAAAGTATGAGGAGATCTTCCAGAAATTTATGATGCTCTGT 2398
OY 1740 TTGATATTTGAAGCAAAAGTGAACCTTCCAGAGCCTGGGGAGTGTGAAGAGACAGATT 1799
DB 2399 TTGATATTTGAAGCAAAAGTGAACCTTCCAGAGCCTGGGGAGTGTGAAGAGACAGATT 2458
OY 1800 CTGTTGACGCTTCCACAGTGCAGAGCTGACAGACTTTGAGTGAAGTACCTTAAGAG 1859
DB 2459 ATGTTGACGCTTCCACAGTGCAGAGCTGACAGACTTTGAGTGAAGTACCTTAAGAG 2518
OY 1860 ATTTCTTTAGAGACTCTGATTTGAATTTGTGTGATGTCACTC - AAAGAAATATATG 1917
DB 2519 ATTTCTTTAGAGAAATCCGATTTGAATTTGTGTGATGTCACTCAGAAAGATCTGAATG 2578
OY 1918 GTATATTTATTAATTTTAAATTTGATATTTGAAATTAATGTAATTTTATATATAA 1977
DB 2579 GTATATTTATTAATTTTAAATTTGATATTTGAAATTAATGTAATTTTATATATAA 2638
OY 1978 AAAAAAAAAAAAAAAAAA 1992
DB 2639 AAAAAAAAAAAAAAAAAA 2653
```

RESULT 8
ABV22873
ID ABV22873 standard: cDNA: 2884 BP.

XX ABV22873;

AC 13-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 22864.

XX Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 XX MO200160860-A2.
 XX 23-AUG-2001.
 XX 20-FEB-2001; 2001MO-US05171.
 XX 17-FEB-2000; 2000US-183319P.
 XX 16-MAR-2000; 2000US-189862P.
 XX 25-MAY-2000; 2000US-207454P.
 XX 09-JUN-2000; 2000US-211314P.
 XX 18-JUL-2000; 2000US-219007P.
 XX 13-DEC-2000; 2000US-255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX Schlegel R, Endege WO, Monahan JE;
 DR WPI; 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 PS Claim 1; Page 4048; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC Sequence 2884 BP; 851 A; 551 C; 684 G; 784 T; 14 other:
 SQ
 Query Match 85.5%; Score 1702.6; DB 23; Length 2884;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 540 CACCACAGATACACCTGGAGAGAGAGTCTCAAGTGTCTCAATGTTGACCTGGCT 599
 DB 1383 CACCACAGATACACCTGGAGAGAGTCTCAAGTGTCTCAATGTTGACCTGGCT 1442
 QY 600 TTACTGGAACTTTTCTACACAAAAGTCAGATGCATCCACTTACCAATGAAGTGA 659
 DB 1443 TTACTGGAACTTTTCTACACAAAAGTCAGATGCATCCACTTACCAATGAAGTGA 1502
 QY 660 CGAATTTTCAATGATAGTACCTCAGAGACAGTGAAGCAACAGATATGTCA 719
 DB 1503 CAAGAATTTTCAATGATAGTACCTCAGAGACAGTGAAGCAACAGATATGTCA 1562
 QY 720 TTCTGGAGGTACACCGGACTCATGGGTGTTGGTGTATGACCTCAGAGTGAGCAG 779
 DB 1563 TTCTGGAGGTACACCGGACTCATGGGTGTTGGTGTATGACCTCAGAGTGAGCAG 1622
 QY 780 CTGTTTTCATGAACTGTGAGAGCTTTTGAACACTGAAAAGAGAGGTGAGACCTA 839
 DB 1623 CTGTTTTCATGAACTGTGAGAGCTTTTGAACACTGAAAAGAGAGGTGAGACCTA 1682
 QY 840 GAAGAACAATTTTGTTCAGAGCTGGGATGCAGAAATTTGCTCTTGGTCTACTG 899
 DB 1683 GAAGAACAATTTTGTTCAGAGCTGGGATGCAGAAATTTGCTCTTGGTCTACTG 1742
 QY 900 AGTGGCAGAGATTAATTCAGACTCTCCAGAGCGTGGCGCTTATTAATGCTG 959
 DB 1743 AGTGGCAGAGATTAATTCAGACTCTCCAGAGCGTGGCGCTTATTAATGCTG 1802
 QY 960 ACTCATCTATAGAAGAACTACACCTGAGAGTTTGTATACACCATGATGTACAGCT 1019
 DB 1803 ACTCATCTATAGAAGAACTACACCTGAGAGTTTGTATACACCATGATGTACAGCT 1862
 QY 1020 TGGTATACACCTTACAAAAGAGCTGAAAGCCCTATGAAAGCTTTGAAGCAATCTC 1079
 DB 1863 TGGTATACACCTTACAAAAGAGCTGAAAGCCCTATGAAAGCTTTGAAGCAATCTC 1922
 QY 1080 TTTATGAAGTTGAGCTTAAAGAGTCTCCCAAGTTCAGTGCATGCCAGATTA 1139
 DB 1923 TTTATGAAGTTGAGCTTAAAGAGTCTCCCAAGTTCAGTGCATGCCAGATTA 1982
 QY 1140 GCAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCAGACCTTGGAAATGCTTCAG 1199
 DB 1983 GCAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCAGACCTTGGAAATGCTTCAG 2042
 QY 1200 GCAGACAGAGTATCTAAAGTTGGGAAACAAGAAATTCAGCGCTTCCACTATTC 1259
 DB 2043 GCAGACAGAGTATCTAAAGTTGGGAAACAAGAAATTCAGCGCTTCCACTATTC 2102
 QY 1260 ACAGTCTATGAAGACATATGAGTGTGGGAAAGTTTATGATCCAAATGTTAAATATC 1319
 DB 2103 ACAGTCTATGAAGACATATGAGTGTGGGAAAGTTTATGATCCAAATGTTAAATATC 2162
 QY 1320 ACCTCACTGTGGCCAGGTTTCAGAGAGAGTGTGTTGAAGTCAAGCAATTCATATGTC 1379
 DB 2163 ACCTCACTGTGGCCAGGTTTCAGAGAGAGTGTGTTGAAGTCAAGCAATTCATATGTC 2222
 QY 1380 TCCCTTTGATGTCAGATTAATGCTGATTTTGAAGATGTCGTGCAAAATGTACA 1439
 DB 2223 TCCCTTTGATGTCAGATTAATGCTGATTTTGAAGATGTCGTGCAAAATGTACA 2282
 QY 1440 ATATTTCTATGAAGATCCACAGGAATATGAACATATGATATTTGATTCCTT 1499
 DB 2283 ATATTTCTATGAAGATCCACAGGAATATGAACATATGATATTTGATTCCTT 2342
 QY 1500 TTTCTGACGTAAGAAATTTTACAGAAATGCTTCCAGTTTCAGCGAGACTCCAGAGCT 1559
 DB 2343 TTTCTGACGTAAGAAATTTTACAGAAATGCTTCCAGTTTCAGCGAGACTCCAGAGCT 2402
 QY 1560 TTGACAAAAGCAACCAATATGTTTAAGATGATGAATGAATCAACATGATTTGAGAA 1619
 DB 2403 TTGACAAAAGCAACCAATATGTTTAAGATGATGAATGAATCAACATGATTTGAGAA 2462
 QY 1620 GAGCATTTATGATTCATTAAGGTATACAGACAGACCTTTTATAGGCATGTCATATATG 1679

Db 2463 GAGCATTATGATCCATTAGGTTACAGACAGGCCCTTTATAGGCATGCTATG 2522
 QY 1680 CTCCAGACGCCACACAGATATGACAGGGAGTCATTCCAGATTTATGATGCTCTGT 1739
 Db 2523 CTCACAGAGCCACACAGATATGACAGGGAGTCATTCCAGATTTATGATGCTCTGT 2582
 QY 1740 TTGATATTGAAGAAGAGTGGAGCCCTTCGAAGGCCCTGGGAGATGTGAAGACAGATT 1799
 Db 2583 TTGATATTGAAGAAGAGTGGAGCCCTTCGAAGGCCCTGGGAGATGTGAAGACAGATT 2642
 QY 1800 CTGTTGACGCTTCACAGTGCAGAGCTGCAGAGACTTGTAGTGAAGTACCTCAAGAG 1859
 Db 2643 ATGTTGACGCTTCACAGTGCAGAGCTGCAGAGACTTGTAGTGAAGTACCTCAAGAG 2702
 QY 1860 ATTTCTTGAAGACTCTGTATTTGAATTTGTGTATGTCACCTC--AAAGATTAATATG 1917
 Db 2703 ATTTCTTGAAGAAATCCGATTTGAATTTGTGTATGTCACCTCAGAAAGATTCGAATG 2762
 QY 1918 GTATATTGATTAATTTTAAATTTGATATTGTAATTAAGTTGAATTTATATATAA 1977
 Db 2763 GTATATTGATTAATTTTAAATTTGATATTGTAATTAAGTTGAATTTATATATAA 2822
 QY 1978 AAAAAAAAAAAAAA 1992
 Db 2823 AAAAAAAAAAAAAA 2837

RESULT 9
 ABV23013
 ID ABV23013 standard; cDNA: 2884 BP.
 XX ABV23013;

DT 13-SEP-2002 (first entry)

XX Human prostate expression marker cDNA 23004.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker.

XX Pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US05171.

XX 17-FEB-2000; 2000US-183319P.

XX 16-MAR-2000; 2000US-189862P.

XX 25-MAY-2000; 2000US-207454P.

XX 09-JUN-2000; 2000US-211314P.

XX 18-JUL-2000; 2000US-219007P.

XX 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of

XX prostate cells and correlating with presence of prostate cancer, useful

XX for detecting presence of prostate cancer, stage of prostate cancer -

XX Claim 1; Page 4097-4098; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising

XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

XX specification or its complement. (I) is useful for:

XX (a) assessing whether a patient is afflicted with prostate cancer;

XX (b) monitoring the progression of prostate cancer in a patient;

CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient; efficacy of a therapy for inhibiting prostate cancer
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) assessing a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX

Sequence 2884 BP; 851 A; 551 C; 684 G; 784 T; 14 other;

Query Match 85.5%; Score 1702.6; DB 23; Length 2884;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 240 AGGTTAAATAGCCAGTGCAGAGGCCAAGAGATCTTACTAGACCCCTGTG 299
 Db 1083 AGGTTAAATAGCCAGTGCAGAGGCCAAGAGATCTTACTAGACCCCTGTG 1142
 QY 300 ACTACTTGTCTCTGGGGTGAAGTCTTATCCAGACGGTTGGAATCTTCTGGAGGTGTG 359
 Db 1143 ACTACTTGTCTCTGGGGTGAAGTCTTATCCAGATGGTGAATCTTCTGGAGGTGTG 1202
 QY 360 TCCAGCGTGAATATCTTAATCTGAATGSGAGAGGCCCTCAGACCGAGTTATCC 419
 Db 1203 TCCAGCGTGAATATCTTAATCTGAATGSGAGAGGCCCTCAGACCGAGTTATCC 1262
 QY 420 CAGCAAAATGATAGCGTTATAGGATGGAATTCAGAGGCTGTTGCTTCCAGATATCC 479
 Db 1263 CAGCAAAATGATAGCGTTATAGGATGGAATTCAGAGGCTGTTGCTTCCAGATATCC 1322
 QY 480 CTGTTTCATCAGTTGATATATGATGACAGAGACTCTTCAAGAAAATGSGTGTGCTAG 539
 Db 1323 CTGTTTCATCAGTTGATATATGATGACAGAGACTCTTCAAGAAAATGSGTGTGCTAG 1382
 QY 540 CACCACCGATAGAGCGTGGAGAGAGTCCAAAGTGTCTTCAATGTTGAGCTGCT 599
 Db 1383 CACCACCGATAGAGCGTGGAGAGAGTCCAAAGTGTCTTCAATGTTGAGCTGCT 1442
 QY 600 TTACTGGAACCTTTCTACACAAAAGTCAAGATGACATCCACTTACCAATGAATGA 659
 Db 1443 TTACTGGAACCTTTCTACACAAAAGTCAAGATGACATCCACTTACCAATGAATGA 1502
 QY 660 CGAGAATTTACAAATGTGATAGTACTCTCAGAGAGCAGTGAACACAGATATATGCA 719
 Db 1503 CAAGAATTTACAAATGTGATAGTACTCTCAGAGAGCAGTGAACACAGATATATGCA 1562
 QY 720 TTCTGGAGGTCACCGGACTCATGGGTGTTGGTATGACCCCTCAGAGTGGAGCAG 779
 Db 1563 TTCTGGAGGTCACCGGACTCATGGGTGTTGGTATGACCCCTCAGAGTGGAGCAG 1622
 QY 780 CTGTTGTTTCATGAACCTTGAGAGCTTTGGAACACTGAAAAAGAGGTTGAGACCTA 839
 Db 1623 CTGTTGTTTCATGAACCTTGAGAGCTTTGGAACACTGAAAAAGAGGTTGAGACCTA 1682
 QY 840 GAAGAACAATTTGTTTCAAGCTGGGATGCAGAGAAATTTGGTCTTCTGTTCTACTG 899
 Db 1683 GAAGAACAATTTGTTTCAAGCTGGGATGCAGAGAAATTTGGTCTTCTGTTCTACTG 1742
 QY 900 AGTGGGAGAGGATTAATTCAGACTCCCTTCAAGAGCCGGGCTGATATTAATGCTG 959
 Db 1743 AGTGGGAGAGGATTAATTCAGACTCCCTTCAAGAGCCGGGCTGATATTAATGCTG 1802
 QY 960 ACTCATCTATGAAGAACTACACTCTGAGAGTTGATTTACACCACTGATGTACAGCT 1019
 Db 1803 ACTCATCTATGAAGAACTACACTCTGAGAGTTGATTTACACCACTGATGTACAGCT 1862
 QY 1020 TGTATACACCTTAACAAAGAGCTGAAGAGCCCTGATGAAGGCTTTGAGGCAATCTC 1079
 Db 1863 TGTATACACCTTAACAAAGAGCTGAAGAGCCCTGATGAAGGCTTTGAGGCAATCTC 1922

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QY 1080 TTTATGAAAGTGGACTATAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCAGATAA 1139
    |||
DB 1923 TTTATGAAAGTGGACTATAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCAGATAA 1982
QY 1140 GCAAATTTGGGATCTGGAATGATTTTGGAGTGTCTTCCAGAGACTTGAATTGGCTTCA 1199
    |||
DB 1983 GCAAATTTGGGATCTGGAATGATTTTGGAGTGTCTTCCAGAGACTTGAATTGGCTTCA 2042
QY 1200 GCAGAGCAGGATATCTAATAAATTTGGGAAACAACAATTCAGCGGCTATCCAGCTATC 1259
    |||
DB 2043 GCAGAGCAGGATATCTAATAAATTTGGGAAACAACAATTCAGCGGCTATCCAGCTATC 2102
QY 1260 ACAGTGTCTATGAACATATGAGTGTGGTGGAAAGTTTATGATCCAAATGTTAAATATC 1319
    |||
DB 2103 ACAGTGTCTATGAACATATGAGTGTGGTGGAAAGTTTATGATCCAAATGTTAAATATC 2162
QY 1320 ACCCTCAGTGGCCCGAGTTCAGAGAGGAGTGTGGTGGAGCTAGCCAAATCCATATGTC 1379
    |||
DB 2163 ACCCTCAGTGGCCCGAGTTCAGAGAGGAGTGTGGTGGAGCTAGCCAAATCCATATGTC 2222
QY 1380 TCCCTTTGATGTGGAGATATATGCTATGCTTTTAAAGAAATGCTGCAAAATCTACA 1439
    |||
DB 2223 TCCCTTTGATGTGGAGATATATGCTATGCTTTTAAAGAAATGCTGCAAAATCTACA 2282
QY 1440 ATATTTCTATGAACATCCACAGAAATGAGACATACAGTTATCATTTGATTCACCTT 1499
    |||
DB 2283 GATTTTCTATGAACATCCACAGAAATGAGACATACAGTTATCATTTGATTCACCTT 2342
QY 1500 TTTTCGACGTAAAAATTTTACAGAAATGCTTCCAGTTCAGCCAGAGATCCAGACT 1559
    |||
DB 2343 TTTTCGACGTAAAAATTTTACAGAAATGCTTCCAGTTCAGTTCAGTTCAGAGACT 2402
QY 1560 TTGACAAAAGCAACCCATATTGTTAAGAAATGATGATGATCAACATGTTTCGGAAA 1619
    |||
DB 2403 TTGACAAAAGCAACCCATATTGTTAAGAAATGATGATGATCAACATGTTTCGGAAA 2462
QY 1620 GAGCATTTATGATCATTAGGTTACACAGAGACCTTTTATAGCATGTCATCTATG 1679
    |||
DB 2463 GAGCATTTATGATCATTAGGTTACACAGAGACCTTTTATAGCATGTCATCTATG 2522
QY 1680 CTCGCAAGCGCCACACAAGATGTCAGAGGGAGTCAATCCAGAAATTTATGATGCTCT 1739
    |||
DB 2523 CTCGCAAGCGCCACACAAGATGTCAGAGGGAGTCAATCCAGAAATTTATGATGCTCT 2582
QY 1740 TTGATATTGAAAGCAAGTGAGACCTTCCAGGCGTGGGAGATGGAAGAGACAGATT 1799
    |||
DB 2583 TTGATATTGAAAGCAAGTGAGACCTTCCAGGCGTGGGAGATGGAAGAGACAGATT 2642
QY 1800 CTGTTGCAGCCTTCACAGTGCAGGAGCTGCAGAGACTTGAAGTGAAGTGAAGG 1859
    |||
DB 2643 ATGTTGCAGCCTTCACAGTGCAGGAGCTGCAGAGACTTGAAGTGAAGTGAAGG 2702
QY 1860 ATTTCTTTAGAGACTGCTATTTGAATTTTGTGTGATGTCTAC--AAAGATTAATATG 1917
    |||
DB 2703 ATTTCTTTAGAGACTGCTATTTGAATTTTGTGTGATGTCTAC--AAAGATTAATATG 2762
QY 1918 GTATATTGATTAATTTTAAATTTGTAATTTTGAATTAAGTTGAATTTATATATATAA 1977
    |||
DB 2763 GTATATTGATTAATTTTAAATTTGTAATTTTGAATTAAGTTGAATTTATATATATAA 2822
QY 1978 AAAAAAAAAAAAAA 1992
    |||
DB 2823 AAAAAAAAAAAAAA 2837

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RESULT 10

ABV28703 standard: cDNA: 2884 BP.

ABV28703:

XX 16-SEP-2002 (first entry)

XX

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DE Human prostate expression marker cDNA 28694.
XX
KW Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene: SS.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PE 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
PS Claim 1; Page 6024-6025; 11750bp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (1) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (1) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 2884 BP; 851 A; 551 C; 684 G; 784 T; 14 other;
XX
Query Match 85.5%; Score 1702.6; DB 23; Length 2884;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;
QY 240 AGTTAAAAATGCCAGCTGCGAGGCGCCAAAGGAGTCAATCTACTACAGACCTGCTG 299
    |||
DB 1083 AGTTAAAAATGCCAGCTGCGAGGCGCCAAAGGAGTCAATCTACTACAGACCTGCTG 1142
QY 300 ACTACTTCTCTCTGGGGTGAAGTCTATTCAGAGCGTTGGATCTTCTGAGAGTGTG 359
    |||
DB 1143 ACTACTTCTCTCTGGGGTGAAGTCTATTCAGAGCGTTGGATCTTCTGAGAGTGTG 1202
QY 360 TCCAGCGTGAATATCTTAATTCGAATGCGAGAGACCTCTCACACAGAGTTACC 419
    |||
DB 1203 TCCAGCGTGAATATCTTAATTCGAATGCGAGAGACCTCTCACACAGAGTTACC 1262
QY 420 CAGCAATGATACGCTTATAGCATGGAATTCAGAGGCTGTGCTTCCAAATATTC 479
    |||
DB 1263 CAGCAATGATATGCTTATAGCGTGAATTCAGAGGCTGTGCTTCCAAATATTC 1322
QY 480 CTGTTCAATCAGTATGATCTATGATGCACAAACCTCTTAATAAAAAATGGGTGGCTCAG 539
    |||
DB 1323 CTGTTCAATCAGTATGATCTATGATGCACAAACCTCTTAATAAAAAATGGGTGGCTCAG 1382

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QY 540 CACCACCATATACAGCTGAGAGAGAGTCTCAAACTGTCTCAATGTTGACCTGGCT 599
 DB 1383 CACCACCATATACAGCTGAGAGAGAGTCTCAAACTGTCTCAATGTTGACCTGGCT 1442
 QY 600 TTCTGGAAATCTTTCTACACAAAAGTCAAGATGCATCCACTCTACCAATGAAGTGA 659
 DB 1443 TTCTGGAAATCTTTCTACACAAAAGTCAAGATGCATCCACTCTACCAATGAAGTGA 1502
 QY 660 CGAGAAATTTACAATGTGATAGTACTCTCAGAGAGAGAGTGAACACAGATATGTCA 719
 DB 1503 CAGAAATTTACAATGTGATAGTACTCTCAGAGAGAGAGTGAACACAGATATGTCA 1562
 QY 720 TTCTGGAGGTCAACCGGACTCATGGGTGTTGGTGTATTGACCTCAAGATGGAGAG 779
 DB 1563 TTCTGGAGGTCAACCGGACTCATGGGTGTTGGTGTATTGACCTCAAGATGGAGAG 1622
 QY 780 CTGTGTCTCAATGAACCTGAGAGAGCTTTGGAACACTGAAAAAGAGGGTGGAGACTA 839
 DB 1623 CTGTGTCTCAATGAACCTGAGAGAGCTTTGGAACACTGAAAAAGAGGGTGGAGACTA 1682
 QY 840 GAAGAACAAATTTGTTTGAAGCTGGAGTCAAGAAATTTGTTGTTGTTCTACTG 899
 DB 1683 GAAGAACAAATTTGTTTGAAGCTGGAGTCAAGAAATTTGTTGTTGTTCTACTG 1742
 QY 900 AGTGGCAGAGAGATATTCAGAGCTCCTCAAGAGCTGGCGTGGCTTATTTATCTG 959
 DB 1743 AGTGGCAGAGAGATATTCAGAGCTCCTCAAGAGCTGGCGTGGCTTATTTATCTG 1802
 QY 960 ACTCATCTATAGAGAGAACTACACTGTGAGTGTATTTGACACCACTGATGACACT 1019
 DB 1803 ACTCATCTATAGAGAGAACTACACTGTGAGTGTATTTGACACCACTGATGACACT 1079
 QY 1020 TGGTATCAACCTTACAAAAGAGCTGAAAAGCCCTGATGAGAGCTTTGAAAGCAATCTC 1079
 DB 1863 TGGTATCAACCTTACAAAAGAGAGCTGAAAAGCCCTGATGAGAGCTTTGAAAGCAATCTC 1922
 QY 1080 TTTATGAAAGTTGGACTTAAAAAAAGTCCCTCCAGAGTTGATGAGTATGCTCCAGATTA 1139
 DB 1923 TTTATGAAAGTTGGACTTAAAAAAAGTCCCTCCAGAGTTGATGAGTATGCTCCAGATTA 1199
 QY 1140 GCAAAATGGGATCTGAAAAATGATTTGAGTGTCTTCCAGAGCTTGAATGCTCTCAG 1199
 DB 1983 GCAAAATGGGATCTGAAAAATGATTTGAGTGTCTTCCAGAGCTTGAATGCTCTCAG 2042
 QY 1200 GCAGAGCAGCGTATCTAAAAATTTGGAAACAAACAAATTCAGCGGCTATCCACTGATC 1259
 DB 2043 GCAGAGCAGCGTATCTAAAAATTTGGAAACAAACAAATTCAGCGGCTATCCACTGATC 2102
 QY 1260 ACAGTGTCTATGAACATATGATGTTGGTGAAGAACTTTTATGATCCATGTTTAAATATC 1319
 DB 2103 ACAGTGTCTATGAACATATGATGTTGGTGAAGAACTTTTATGATCCATGTTTAAATATC 2162
 QY 1320 ACCTCAGTGGCCAGGTTGAGAGAGAGTGTGTTGAGCTGAGCCATTCATAGTGC 1379
 DB 2163 ACCTCAGTGGCCAGGTTGAGAGAGAGTGTGTTGAGCTGAGCCATTCATAGTGC 2222
 QY 1380 TCCCTTTGATTTGAGATTTATGCTGATTTTAAAGAAATGCTGACAAAATCTACA 1439
 DB 2223 TCCCTTTGATTTGAGATTTATGCTGATTTTAAAGAAATGCTGACAAAATCTACA 2282
 QY 1440 ATATTTCTATGAACATCTACAGAAATGAAGACATACAGTTTATCATTTTATTCACCTT 1499
 DB 2283 GTATTTCTATGAACATCTACAGAAATGAAGACATACAGTTTATCATTTTATTCACCTT 2342
 QY 1500 TTCTGCGATGAAAAATTTTACAGAAATGCTTCCCAATTCAGAGAGAGCTCCAGAGCT 1559
 DB 2343 TTCTGCGATGAAAAATTTTACAGAAATGCTTCCCAATTCAGAGAGAGCTCCAGAGCT 2402
 QY 1560 TTGACAAAAGCACCACATATTTGTAAGATGATGATCACTCATGTTTCTGAAA 1619
 DB 2403 TTGACAAAAGCACCACATATTTGTAAGATGATGATCACTCATGTTTCTGAAA 2462

QY 1620 GAGCATTTATTTGATTCATTAGGGTTACAGACAGACCTTTTATAGCATGTCATCTATG 1679
 DB 2463 GAGCATTTATTTGATTCATTAGGGTTACAGACAGACCTTTTATAGCATGTCATCTATG 2522
 QY 1680 CTCGAAGCAGCCACAACATATGACAGGAGTCAATCCAGAAATTTATGATGCTCTGT 1739
 DB 2523 CTCGAAGCAGCCACAACATATGACAGGAGTCAATCCAGAAATTTATGATGCTCTGT 2582
 QY 1740 TTGATTTGAAACCAAGTGGAGCTTCCAGAGCTGGGGAGTGAAGACAGATTT 1799
 DB 2583 TTGATTTGAAACCAAGTGGAGCTTCCAGAGCTGGGGAGTGAAGACAGATTT 2642
 QY 1800 CTGTCAGCCTTCACAGTGCAGAGCTGACAGAGCTTTGACTGAAGTGAAGCTTAAGAG 1859
 DB 2643 ATGTCAGCCTTCACAGTGCAGAGCTGACAGAGCTTTGACTGAAGTGAAGCTTAAGAG 2702
 QY 1860 ATTCTTGAAGACTCTGATTTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1917
 DB 2703 ATTCTTGAAGACTCTGATTTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2762
 QY 1918 GTATATGATTAATTTTAAATTTGATATTTGAAATTAAGTTGAATTTATATATAA 1977
 DB 2763 GTATATGATTAATTTTAAATTTGATATTTGAAATTAAGTTGAATTTATATATAA 2822
 QY 1978 AAAAAAAAAAAAAA 1992
 DB 2823 AAAAAAAAAAAAAA 2837
 RESULT 11
 ID ABY28849 standard; cDNA; 2884 BP.
 AC ABY28849:
 XX 16-SEP-2002 (first entry)
 DT 16-SEP-2002 (first entry)
 XX Human prostate expression marker cDNA 28840.
 DE Human prostate cancer: cytostatic; carcinogen: pharmacodynamic marker:
 XX human: prostate cancer: cytostatic; carcinogen: pharmacodynamic marker:
 KW pharmacogenomic marker; gene: ss.
 OS Homo sapiens.
 XX Homo sapiens.
 PN WO200160860-A2.
 XX 23-AUG-2001.
 PD 20-FEB-2001; 2001WO-US05171.
 PF 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189863P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 PI Schlegel R, Endege WO, Monahan JE;
 XX WPI: 2001-662795/76.
 DR Novel isolated nucleic acid molecule associated with cancerous state of
 XX prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1: Page 6076-6077; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABY00010-ABY62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 2884 BP; 851 A; 551 C; 684 G; 784 T; 14 other;

Query Match 85.5%; Score 1702.6; DB 23; Length 2884;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 240 AGGTTAAATGCCCCAGCTGGAGGGCCAAAGAGTCATCTCTACTAGACCCCTCTG 289
 DB 1083 AGGTTAAATGCCCCAGCTGGAGGGCCAAAGAGTCATCTCTACTAGACCCCTCTG 1142
 QY 300 ACTACTTTGCTCTGGGGTGAAGTCTATCCAGACGGTTGGAATCTCTGAGAGTGTG 359
 DB 1143 ACTACTTTGCTCTGGGGTGAAGTCTATCCAGATGGTGAATCTCTGAGAGTGTG 1202
 QY 360 TCCAGCGTGAATATCCCTAAATCTGAATGTGTCAGAGACCCCTCCACCCAGTTACC 419
 DB 1203 TCCAGCGTGAATATCCCTAAATCTGAATGTGTCAGAGACCCCTCCACCCAGTTACC 1262
 QY 420 CAGCAATGATAGCGTTATAGGCAATGGAATGTCAGAGCGTGTGCTCTCCAGATATTC 479
 DB 1263 CAGCAATGATAGCGTTATAGGCGTGAATGTCAGAGCGTGTGCTCTCCAGATATTC 1322
 QY 480 CTGTTCATCAGTTGGATATGATGATGACAGAGACCTCCAGAAAAAATGGGTGCTCAG 539
 DB 1323 CTGTTCATCAGTTGGATATGATGATGACAGAGACCTCCAGAAAAAATGGGTGCTCAG 1382
 QY 540 CACACACAGATACAGCTGAGAGGAAGTCTCAAGTGTCTCAATGTTGGACCTGGCT 599
 DB 1383 CACACACAGATACAGCTGAGAGGAAGTCTCAAGTGTCTCAATGTTGGACCTGGCT 1442
 QY 600 TTACTGGAACCTTTTCTACCAAAAAAGTCAAGATGACATCCACTTACCAATGAAGTGA 659
 DB 1443 TTACTGGAACCTTTTCTACCAAAAAAGTCAAGATGACATCCACTTACCAATGAAGTGA 1502
 QY 660 CGAGATTTTCAATGATGATGATGATCTCTCAGAGAGCAGTGAACACAGAGATATGTCA 719
 DB 1503 CGAGATTTTCAATGATGATGATGATCTCTCAGAGAGCAGTGAACACAGAGATATGTCA 1562
 QY 720 TTCTGGAGGTCAACCGGAGCTCAATGGGTGTTGGTGTATGACCCCTCAAGTGGAGCAG 779
 DB 1563 TTCTGGAGGTCAACCGGAGCTCAATGGGTGTTGGTGTATGACCCCTCAAGTGGAGCAG 1622
 QY 780 CTGTGTTTCAAGAACTGTGAGAGAGCTTTTGAACACTGAAAGAAAGAGGTGAGACCTA 839
 DB 1623 CTGTGTTTCAAGAACTGTGAGAGAGCTTTTGAACACTGAAAGAAAGAGGTGAGACCTA 1682
 QY 840 GAAGAACAAATTTGTTTGGCAAGCTGGATGACAGAAAGATTTGGTCTTGTGTTTACTG 899
 DB 1683 GAAGAACAAATTTGTTTGGCAAGCTGGATGACAGAAAGATTTGGTCTTGTGTTTACTG 1742
 QY 900 AGTGGGAGAGATATTCAGAGCTCCTTCAAGAGGTGGCGGTATATTAATGCTG 959
 DB 1743 AGTGGGAGAGATATTCAGAGCTCCTTCAAGAGGTGGCGGTATATTAATGCTG 1802
 QY 960 ACTCATCTATAGAAGAACTACACTGTGAGTTGATTTATACCACTGATGTACAGCT 1019
 DB 1803 ACTCATCTATAGAAGAACTACACTGTGAGTTGATTTATACACGCGTATGTACAGCT 1862
 QY 1020 TGGTATACAACTTAACAAAAGAGCTGAAAAGCCCTGATGAGAGCTTTGAAGCAATCTC 1079
 DB 1863 TGGTATACAACTTAACAAAAGAGCTGAAAAGCCCTGATGAGAGCTTTGAAGCAATCTC 1922

QY 1080 TTTATGAAGTGGAGTAAAAAAGTCCCTCCAGAGTTCAGTGCAGTCCAGATTA 1139
 DB 1923 TTTATGAAGTGGAGTAAAAAAGTCCCTCCAGAGTTCAGTGCAGTCCAGATTA 1982
 QY 1140 GCAAAATGGGATCGGAATGATTTGAGGTGTTCTTCCAGACACTTGAATGCTTCAG 1199
 DB 1983 GCAAAATGGGATCGGAATGATTTGAGGTGTTCTTCCAGACACTTGAATGCTTCAG 2042
 QY 1200 GCAGAGCAGGTATCTAAATAATTTGGGAAACAAATTCACGGCTATCCACTATC 1259
 DB 2043 GCAGAGCAGGTATCTAAATAATTTGGGAAACAAATTCACGGCTATCCACTATC 2102
 QY 1260 ACAGTGTCTATGAACATATGAGTGTGTGGAAGATTTATGATCCAAATTTAAATATC 1319
 DB 2103 ACAGTGTCTATGAACATATGAGTGTGTGGAAGATTTATGATCCAAATTTAAATATC 2162
 QY 1320 ACCCTACGTGAGCCAGGTTGAGAGAGGATGGTGTGAGCTAAGCAATTCATAGTGC 1379
 DB 2163 ACCCTACGTGAGCCAGGTTGAGAGAGGATGGTGTGAGCTAAGCAATTCATAGTGC 2222
 QY 1380 TCCCTTTGATTTGTGAGATTTATGCTGTAGTATTTAAGAAATGCTGACAAATCTACA 1439
 DB 2223 TCCCTTTGATTTGTGAGATTTATGCTGTAGTATTTAAGAAATGCTGACAAATCTACA 2282
 QY 1440 ATATTTCTATGAACATCCACAGGAATGAAGACATTCAGTTATCATTTGATCTACTT 1499
 DB 2283 ATATTTCTATGAACATCCACAGGAATGAAGACATTCAGTTATCATTTGATCTACTT 2342
 QY 1500 TTTCTGAGTAAAAAATTTTACAGAAATTCCTTCCAAAGTTCAGAGAGAGCTCCAGACT 1559
 DB 2343 TTTCTGAGTAAAAAATTTTACAGAAATTCCTTCCAAAGTTCAGAGAGAGCTCCAGACT 2402
 QY 1560 TTGACAAACCAACCAATATTTGTTAAGATGATGAATGATCAACTCATGTTCTGAAA 1619
 DB 2403 TTGACAAACCAACCAATATTTGTTAAGATGATGAATGATCAACTCATGTTCTGAAA 2462
 QY 1620 GAGCATTTATGATCCATTTAGGGTTACACAGACAGCTTTTTPAGGATGATCATATG 1679
 DB 2463 GAGCATTTATGATCCATTTAGGGTTACACAGACAGCTTTTTPAGGATGATCATATG 2522
 QY 1680 CTCCAAGCAGCCACACAACTATGCAAGGGAGTCAATCCAGGAATTTATGATGCTCTGT 1739
 DB 2523 CTCCAAGCAGCCACACAACTATGCAAGGGAGTCAATCCAGGAATTTATGATGCTCTGT 2582
 QY 1740 TTGATATTTGAAGCAAGTGGACCTTCCAGAGCTTGGGAGATGTGAAGACAGATTT 1799
 DB 2583 TTGATATTTGAAGCAAGTGGACCTTCCAGAGCTTGGGAGATGTGAAGACAGATTT 2642
 QY 1800 CTGTGAGGCTTTCACAGTGTGAGAGCTGACAGAGCTTTGAGTGAAGTGGCTAAGAG 1859
 DB 2643 ATGTGAGGCTTTCACAGTGTGAGAGCTGACAGAGCTTTGAGTGAAGTGGCTAAGAG 2702
 QY 1860 ATTCTTTAGAGCTCTGATTTGAATTTGCTGTATGTCTACTC - AAAGAAATATATG 1917
 DB 2703 ATTCTTTAGAGCTCTGATTTGAATTTGCTGTATGTCTACTC - AAAGAAATATATG 2762
 QY 1918 GTATATTTGAATTTTAAATTTGATATTTTGAATTAAGTGAATATATATATAA 1977
 DB 2763 GTATATTTGAATTTTAAATTTGATATTTTGAATTAAGTGAATATATATATAA 2822
 QY 1978 AAAAAAAAAAAAAA 1992
 DB 2823 AAAAAAAAAAAAAA 2837

RESULT 12
 AAT36785
 ID AAT36785 standard; cDNA; 2654 BP.
 AC AAT36785;
 XX
 DT 04-NOV-1996 (first entry)

XX DE Prostate-specific membrane antigen cDNA.
XX KM Prostate-specific membrane antigen; PSM; promoter; prostate cancer;
XX KM metastasis; gene therapy; diagnosis; ss.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FH 1..261
FT 5'UTR /*tag= a
FT CDS 262..2253
FT /*tag= b
FT /*tag= c
FT misc_feature /product= PSM antigen
FT 114..380
FT /*tag= c
FT /*note= "bases 114-380 (-147 to +109) are absent
FT in PSM' cDNA"
FT polyA_signal 2352..2357
FT /*tag= d
XX PD WO9626272-A1.
XX PD 29-AUG-1996.
XX PF 23-FEB-1996; 96WO-US02424.
XX XX 02-JUN-1995; 95US-0470735.
XX PR 24-FEB-1995; 95US-0394152.
XX PR 02-JUN-1995; 95US-0466381.
XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX PI Fair WR, Heston MDW, Israeli RS;
XX WPI: 1996-402365/40.
XX DR P-PSDB; AAM02234.
XX DR
XX PT DNA encoding alternatively spliced prostate-specific membrane
PT antigen - useful to develop prods. for detecting haematogenous
PT micrometastatic tumour cells, or prostate cancer progression
XX PS Example 1; Fig 47A-D: 284pp; English.
XX CC A CDNA clone (AAT36785) codes for human 100 kDa prostate-specific
CC membrane (PSM) antigen (AAM02234), an integral membrane glycoprotein
CC that is very highly expressed in prostatic tumours and metastases.
CC It was obtd. from lymph node carcinoma of prostate (LNCap) cell
CC mRNA by PCR amplification (see also AAT36795-808) and screening of an
CC LNCap cDNA library using an amplified cDNA partial clone as probe.
CC The cDNA can be used to provide probes and primers useful e.g. in
CC detecting haematogenous micrometastatic tumour cells and determining
CC prostate cancer progression (see also AAT36827-30 and AAT36813-18),
CC and in gene therapy. An alternatively spliced PSM, PSM', has a
CC shorter cDNA sequence. PSM genomic DNA is given in AAT36786.
XX CC
XX Sequence 2654 BP; 782 A; 525 C; 639 G; 708 T; 0 other;
Query Match 84.8%; Score 1690; DB 17; Length 2654;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1728; Conservative 0; Mismatches 25; Indels 3; Gaps 2;
QY 240 AGGTTAAAAATGCCAGCTGCGAGGGGCCAAAGAGTCAATTCCTACTCAGACCTGCTG 299
DB 899 AGGTTAAAAATGCCAGCTGCGAGGGGCCAAAGAGTCAATTCCTACTCAGACCTGCTG 958
QY 300 ACTACTTGTCTCTGGGGTGAAGTCTCTATCCAGAGGTTGAATCTTCTGGAGGGTGG 359
DB 959 ACTACTTGTCTCTGGGGTGAAGTCTCTATCCAGATGGTGGAACTTCTCTGGAGGGTGG 1018
QY 360 TCCACGCTGGAATATCCATAATCTGAATGTGTCAGAGAGACCCCTTCACACCGAGTTACC 419
DB 1019 TCCACGCTGGAATATCCATAATCTGAATGTGTCAGAGAGACCCCTTCACACCGAGTTACC 1078

QY 420 CAGCAATGATATAGCGCTTATAGCATGGAATTCAGAGGCTGTGGCTTCCAGTATTC 479
DB 1079 CAGCAATGATATAGCGCTTATAGCGCTGGAATTCAGAGGCTGTGGCTTCCAGTATTC 1138
QY 480 CTGTTCATCCAGTTGGATCTATGATGACACAGAGCTCTAGAAAAAATGGTGGCTCAG 539
DB 1139 CTGTTCATCCAGTTGGATCTATGATGACACAGAGCTCTAGAAAAAATGGTGGCTCAG 1198
QY 540 CACCACCAGATAGCAGCTGGAGAGAGATCTCAAGTGTCTCAATGTTGGACCTGGCT 599
DB 1199 CACCACCAGATAGCAGCTGGAGAGAGATCTCAAGTGTCTCAATGTTGGACCTGGCT 1258
QY 600 TTACTGGAACCTTTCTACACAAAAGTCAAGATGACATCTCACTTACCAATGAAGTGA 659
DB 1259 TTACTGGAACCTTTCTACACAAAAGTCAAGATGACATCTCACTTACCAATGAAGTGA 1318
QY 660 CGAGAAATTTCAATGTGATAGTACTCTCAGAGAGAGCTGGAACCCAGACATATGTCA 719
DB 1319 CAAGAAATTTCAATGTGATAGTACTCTCAGAGAGAGCTGGAACCCAGACATATGTCA 1378
QY 720 TTCTGGAGAGTCAACCGGACTCATGGGTGTTGGTGTATTTGACCCCTCAGAGTGGACAG 779
DB 1379 TTCTGGAGAGTCAACCGGACTCATGGGTGTTGGTGTATTTGACCCCTCAGAGTGGACAG 1438
QY 780 CTGTTGTTCAATGAACCTGTGAGAGCTTTGGAACCTGAAAAGAGGGTGGAGACTA 839
DB 1439 CTGTTGTTCAATGAACCTGTGAGAGCTTTGGAACCTGAAAAGAGGGTGGAGACTA 1498
QY 840 GAAGAACAAATTTGTTTGGCAAGCTGGGATGACAGAAATTTGTTGTTGGTCTCTCTG 899
DB 1499 GAAGAACAAATTTGTTTGGCAAGCTGGGATGACAGAAATTTGTTGTTGGTCTCTCTG 1558
QY 900 AGTGGCAGAGAGATTAATTCAGAGCTCCTTCAAGAGCTGGCGCTTATATTAATGCTG 959
DB 1559 AGTGGCAGAGAGATTAATTCAGAGCTCCTTCAAGAGCTGGCGCTTATATTAATGCTG 1618
QY 960 ACTCATCTATGAGAGAACTACACTCTGAGAGTTGATGTACACACTGATGTACAGCT 1019
DB 1619 ACTCATCTATGAGAGAACTACACTCTGAGAGTTGATGTACACACTGATGTACAGCT 1678
QY 1020 TGGTATACAAACCTTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAATCTC 1079
DB 1679 TGGTATACAAACCTTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAATCTC 1738
QY 1080 TTTATGAAAGTTGAGACTTAATAAAGTCTCTCCAGAGTTAGGGCATGCCAGATTA 1139
DB 1739 TTTATGAAAGTTGAGACTTAATAAAGTCTCTCCAGAGTTAGGGCATGCCAGATTA 1798
QY 1140 GCAAAATGGAGTCTGAAATGATTTTGAAGTGTCTTCCAAAGCACTTGAATGCTTCAG 1199
DB 1799 GCAAAATGGAGTCTGAAATGATTTTGAAGTGTCTTCCAAAGCACTTGAATGCTTCAG 1858
QY 1200 GCAGAGCAGGTAATCTAATAAATTTGGGAACAACAATAATTAGGGGCTATCCACTGATTC 1259
DB 1859 GCAGAGCAGGTAATCTAATAAATTTGGGAACAACAATAATTAGGGGCTATCCACTGATTC 1918
QY 1260 ACAGTGTATGAACAATATAGTATGTTGGAAGTATTTATGATCAATGTTTAAATATC 1319
DB 1919 ACAGTGTATGAACAATATAGTATGTTGGAAGTATTTATGATCAATGTTTAAATATC 1978
QY 1320 ACCTCAGTGTGGCCAGGTTGAGAGAGAGATGTTTGAAGTATCCCAATTCATAGTGC 1379
DB 1979 ACCTCAGTGTGGCCAGGTTGAGAGAGAGATGTTTGAAGTATCCCAATTCATAGTGC 2038
QY 1380 TCCCTTTGATTTGAGATTAATGCTGATGTTTAAAGAACTATGCTACAAAAATCTTCA 1439
DB 2039 TCCCTTTGATTTGAGATTAATGCTGATGTTTAAAGAACTATGCTACAAAAATCTTCA 2098
QY 1440 ATATTTCATGAATAATCCACAGGAATGAAGACATTAAGTTTATCATTTGATTCACCTT 1499
DB 2099 ATATTTCATGAATAATCCACAGGAATGAAGACATTAAGTTTATCATTTGATTCACCTT 2158

Db 1301 TTCTGGAGGTCACCGGAGCTCACTGGGTGTTGGTGTATTGACCCCTCAGAGTGGAGCAG 1360
QY 780 CTGTGTTTCATGAAGTGTGAGAGCTTTTGAACACTGAAGAGAGAGGGTGGAGACCTA 839
Db 1361 CTGTGTTTCATGAAGTGTGAGAGCTTTGGAACACTGAAGAGAGAGGGTGGAGACCTA 1420
QY 840 GAAGACAAATTTGTTGGCAAGCTGGGATCGAGAGAAATTTGGCTCTTGTTGTTCTCTG 899
Db 1421 GAAGAACAAATTTGTTGGCAAGCTGGGATCGAGAGAAATTTGGCTCTTGTTGTTCTCTG 1480
QY 900 AGTGGGAGAGGAAATTTCAAGACTCCTCAAGAGCTGGGCGTCTTATATTATCTG 959
Db 1481 AGTGGGAGAGGAAATTTCAAGACTCCTCAAGAGCTGGGCGTCTTATATTATCTG 1540
QY 960 ACTCATCTATAGAAGAACTACACTCTGAGAGTTGATTTGACACACTGATGTACAGT 1019
Db 1541 ACTCATCTATAGAAGAACTACACTCTGAGAGTTGATTTGACACCCCTGATGTACAGT 1600
QY 1020 TGTATATCAACCTTACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAATCTC 1079
Db 1601 TGTATATCAACCTTACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAATCTC 1660
QY 1080 TTTATGAAGTTGGACTAAAAAAGTCCTCCAGAGTTCCAGTGGCATGCCAGATAA 1139
Db 1661 TTTATGAAGTTGGACTAAAAAAGTCCTCCAGAGTTCCAGTGGCATGCCAGATAA 1720
QY 1140 GCAAAATTTGGATCTGAAAATGATTTTGAAGTGTCTTCCAAAGACTTGAATTCCTTCAG 1199
Db 1721 GCAAAATTTGGATCTGAAAATGATTTTGAAGTGTCTTCCAAAGACTTGAATTCCTTCAG 1780
QY 1200 GCAGACACAGGTATACATAAATTTGGCAACAAATTTAGGGGCTATCCACTGTATC 1259
Db 1781 GCAGACACAGGTATACATAAATTTGGCAACAAATTTAGGGGCTATCCACTGTATC 1840
QY 1260 ACAGTGTCTATGAAGAACTATGATGTGGTGAAGAAAGTTTATGACCAATGTTTAAATTC 1319
Db 1841 ACAGTGTCTATGAAGAACTATGATGTGGTGAAGAAAGTTTATGACCAATGTTTAAATTC 1900
QY 1320 ACCTCACTGTGGCCAGGTTGAGAGAGGATGTGTGTTGAGCTAGCCAAATTCATGTGC 1379
Db 1901 ACCTCACTGTGGCCAGGTTGAGAGAGGATGTGTGTTGAGCTAGCCAAATTCATGTGC 1960
QY 1380 TCCCTTTGATGTGCGAGATATATGCTGTAGTTTAAAGAAATGATGTCGACAAATCTACA 1439
Db 1961 TCCCTTTGATGTGCGAGATATATGCTGTAGTTTAAAGAAATGATGTCGACAAATCTACA 2020
QY 1440 ATATTTCTATGAACATCCACAGAGAAATGAAGACATACAGTTTATCATTTGATTCACCTT 1499
Db 2021 GTATTTCTATGAACATCCACAGAGAAATGAAGACATACAGTTTATCATTTGATTCACCTT 2080
QY 1500 TTTCTGCAGTAAAAAATTTTACAGAAATGCTTCCAGTTACGCGAGAGACTCCAGGACT 1559
Db 2081 TTTCTGCAGTAAAAAATTTTACAGAAATGCTTCCAGTTACGCGAGAGACTCCAGGACT 2140
QY 1560 TTGCAAAAGCAACCAATATTTGTAAGATGATGAATGATCAATCACTGTTTCGAAA 1619
Db 2141 TTGCAAAAGCAACCAATATTTGTAAGATGATGAATGATCAATCACTGTTTCGAAA 2200
QY 1620 GAGCATTTATGATCATTTAGGTTACAGACAGACTTTTATAGCATGTCACTATG 1679
Db 2201 GAGCATTTATGATCATTTAGGTTACAGACAGGCTTTTATAGCATGTCACTATG 2260
QY 1680 CTCACAGAGCCACAAAGATATGAGAGGAGTCAATCCAGGAATTTATGATGCTCTGT 1739
Db 2261 CTCACAGAGCCACAAAGATATGAGAGGAGTCAATCCAGGAATTTATGATGCTCTGT 2320
QY 1740 TTGATATTGAAGCAAAAGTGAACCTTCCAGGCTGGGAGATGTGAAGAGACGATTT 1799
Db 2321 TTGATATTGAAGCAAAAGTGAACCTTCCAGGCTGGGAGATGTGAAGAGACGATTT 2380
QY 1800 CTGTTGACGACCTTCAGATGACGAGCTGACAGAGACTTTGATGAAGTAAAGCTTAAGAG 1859
Db 2381 ATGTTGACGACCTTCAGATGACGAGCTGACAGAGACTTTGATGAAGTAAAGCTTAAGAG 2440

QY 1860 ATTCTTTAGAGACTCTGATTAATTTGCTGATGTACCTC--AAAGATAATAATG 1917
Db 2441 ATTTTATAGGAATCCGATATGATTTGCTGATGTCACTGAGAAAGATCTATATG 2500
QY 1918 GTATATTGATAAATTTTAAATTTGATATTGAAATTAAGTTGAATATTATATATAA 1975
Db 2501 GTATATTGATAAATTTTAAATTTGATATTGAAATTAAGTTGAATATTATATATAA 2558

RESULT 14
AAS45976
ID AAS45976 standard; cDNA; 2558 BP.
XX AAS45976;
AC
XX
DT 18-DEC-2001 (first entry)
XX
DE Human DNA encoding PRO polypeptide sequence #52.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN M020016848-f2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.
XX
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189328P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 21-MAR-2000; 2000US-194647P.
PR 28-MAR-2000; 2000US-194647P.
PR 11-APR-2000; 2000US-195875P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199654P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.

XX (GETH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski RJ, Gurney AL,
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX WPI; 2001-602746/68.
 DR P-PSDB; AA029075.
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumours, such as prostate and breast tumours, in mammals and
 PT to screen for modulators of the compounds -
 PS
 PS Claim 2: Fig 103; 774pp; English.
 XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
 CC primers for PRO polypeptides of the invention. The sequences of the
 CC invention can be used to detect the presence of a tumour in a mammal by
 CC comparing the level of expression of a PRO polypeptide in a test sample
 CC of cells from the animal and a control sample of normal cells, whereby a
 CC higher level of expression in the test sample indicates the presence of a
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human
 CC blood, when contacted with it. A specific polypeptide can be used to
 CC stimulate the proliferation or differentiation of chondrocyte cells. The
 CC PRO proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders.
 XX
 SQ Sequence 2558 BP; 745 A; 509 C; 623 G; 681 T; 0 other;
 Query Match 84.7%; Score 1687.2; DB 22; Length 2558;
 Best Local Similarity 98.6%; Pred. No. 0;
 Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;
 QY 240 AGGTTAAATGCGCCAGCTGCGAGGGGCCAAAGAGTCAATCTCTACAGACCCGCTG 299
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 DB 1301 TTCTGGAGAGTACCGGGAGTCAATGGGTGTTGGTGTATTGACCTCAGAGTGAGCAG 1360

QY 780 CTGTTGTCATGAACCTGTGAGAGCTTTGGAACACTGAAAAAGAGGGTGAGACCTA 839
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 DB 2381 CTGTTGACGCTTTCACAGTGCAGAGCTGCAAGAGCTTTGAGTGAAGTGAAGCTAAGAG 2440

PR 11-JUN-1998; 9805-088863P.
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 PR 10-SEP-1998; 9805-099754P.
 PR 10-SEP-1998; 9805-099763P.
 PR 10-SEP-1998; 9805-099812P.

Query Match 84.7%; Score 1687.2; DB 25; Length 2558;
 Best Local Similarity 98.6%; Pred. No. 0;
 Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

QY 240 AGGTTAAATGCCCCAGCTGGCAGGCGCCAAAGAGATCTTCTTCTACAGACCCCTGCTG 299
 DB 821 AGGTTAAATGCCCCAGCTGGCAGGCGCCAAAGAGATCTTCTTCTACCGACCCCTGCTG 880

QY 300 ACTACTTGTCTCTCTGGGGTGAAGTCTCTATCCAGACGGTTGGAATCTTCTGGAGGTGTC 359
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 DB 1061 CTGTTCATCAGTGTATCTATATGATGCACAGAGCTCTAGAAAAATGGGTGCTCAG 1120
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 QY 600 TTACTGGAACCTTTTCTACACAAAAAGTCAAGTGCATCTTACCAATGAAGTGA 659
 DB 1181 TTACTGGAACCTTTTCTACACAAAAAGTCAAGTGCATCTTACCAATGAAGTGA 1240
 QY 660 CGAGAAATTTACATGTGATAGTACTCTCAGAGACAGTGGAAACAGATATGTCA 719
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 QY 720 TTCTGGAGGTACCGGGACTCATGGGTGTTGGTGTATTAACCTCAGAGTGAAGCAG 779
 DB 1301 TTCTGGAGGTACCGGGACTCATGGGTGTTGGTGTATTAACCTCAGAGTGAAGCAG 1360
 QY 780 CTGTTTGTATGAACCTGTGAGAGCTTTGGAACCTGAAAAAGAGGTGAGACCTTA 839
 DB 1361 CTGTTTGTATGAACCTGTGAGAGCTTTGGAACCTGAAAAAGAGGTGAGACCTTA 1420
 QY 840 GAAGAACAAATTTGTTGGAAGCTGGAGTGCAGAAATTTGGTCTTGGTCTACAG 899
 DB 1421 GAAGAACAAATTTGTTGGAAGCTGGAGTGCAGAAATTTGGTCTTGGTCTACAG 1480
 QY 900 AGTGGCAGAGGATAATTCAGACTCTTCAAGAGCGTGGCTTATATTAATGCTG 959
 DB 1481 AGTGGCAGAGGATAATTCAGACTCTTCAAGAGCGTGGCTTATATTAATGCTG 1540
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 QY 1140 GCAAATTTGGATCTGAAATGATTTGAGGTCTTCTCAAGACACTTGAATTCCTTCG 1199
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 DB 1901 ACCTGCTGTGGCCCGGTTTCGAGAGGAGATGTTTATAGCTAGCCAAATTCATATGTC 1960

RT "Molecular characterization of human brain N-acetylated alpha-linked
CC acidic dipeptidase (NALADase)."
RL J. Pharmacol. Exp. Ther. 286:1020-1025(1998).
[6]
RP SEQUENCE FROM N.A. (ISOFORM PSMA-1), AND CHARACTERIZATION.
RC TISSUE-PROSTATE;
RX MEDLINE=99185063; PubMed=10085079;
RA Pargalos M.N., Neefs J.-M., Somers M., Verhasselt P., Bekkers M.,
van der Helm L., Fraiponts E., Ashton D., Gordon R.D.;
RT "Isolation and expression of novel human glutamate carboxypeptidases
with N-acetylated alpha-linked acidic dipeptidase and dipeptidyl
RL peptidase IV activity.";
J Biol. Chem. 274:8470-8483(1999).
[7]
RP SEQUENCE FROM N.A. (ISOFORMS PSMA-1 AND PSMA-2), AND VARIANT HHC
RP TYR-475.
RC TISSUE=Jejunum;
RX MEDLINE=20545101; PubMed=11092759;
RA Devlin A.M., Ling E.-H., Pearson J.M., Fernando S., Clarke R.,
Smith A.D., Halsted C.H.;
RT "Glutamate carboxypeptidase II: a polymorphism associated with lower
Hum. Mol. Genet. 9:2837-2844(2000).
[8]
RP SEQUENCE FROM N.A. (ISOFORM PSMA-5).
RA Pearce D.D., Zhang Y., Holt G., Ferrer K.T., Heller M., Sosman J.A.,
Xue B.H.;
RT "Identification of three novel splice variants of prostate-specific
membrane antigen.";
Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
[9]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS PSMA-3 AND PSMA-4).
RA Lupold S.E., Griley S.C., Coffey D.S.;
RT "Alternative splicing of the prostate-specific membrane antigen.";
Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[10]
RP SEQUENCE OF 60-74, AND SUBCELLULAR LOCATION.
RC TISSUE=Prostatic carcinoma;
RX MEDLINE=99028849; PubMed=9809977;
RA Grauer L.S., Lawler K.D., Maignac J.L., Kumar A., Goel A.S.,
Wolfe R.L.;
RT "Identification, purification, and subcellular localization of
prostate-specific membrane antigen PSM' protein in the LNCaP prostatic
carcinoma cell line.";
Cancer Res. 58:4787-4789(1998).
[11]
RP ALTERNATIVE SPLICING.
RA Bzdega T., She D., Turli T., Wroblewska B., Neale J.H.;
RT "Molecular cloning of alternatively spliced variants of the peptidase
against N-acetylasparylglutamate (NAAG) from human and rat nervous
systems.";
Abstr. Soc. Neurosci. 24:579-579(1998).
[12]
RP CHARACTERIZATION.
RX MEDLINE=98288196; PubMed=9622670;
RA Luthi-Carter R., Barczak A.K., Speno H.D., Coyle J.T.;
RT "Hydrolysis of the neuropeptide N-acetylasparylglutamate (NAAG) by
cloned human glutamate carboxypeptidase II.";
Brain Res. 795:341-348(1998).
[13]
RP DOMAIN STRUCTURE.
RX MEDLINE=97330810; PubMed=9187245;
RA Rawlings N.D., Barrett A.J.;
RT "Structure of membrane glutamate carboxypeptidase.";
Biochim. Biophys. Acta 1339:247-252(1997).
[14]
RP MUTAGENESIS.
RX MEDLINE=99102317; PubMed=9882712;
RA Speno H.S., Luthi-Carter R., Macias W.L., Valentine S.L.,
Josh A.R.T., Coyle J.T.;
RT "Site-directed mutagenesis of predicted active site residues in
glutamate carboxypeptidase II.";
Mol. Pharmacol. 55:179-185(1999).
[15]
CC -1- FUNCTION: Has both folate hydrolase and N-acetylated-alpha-linked-
CC acidic dipeptidase (NALADase) activity. Has a preference for tri-
CC alpha-glutamate peptides. In the intestine, required for the
CC uptake of folate. In the brain, modulates excitatory
CC neurotransmission through the hydrolysis of the neuropeptide, N-
CC acetylasparylglutamate (NAAG), thereby releasing glutamate. Stable
CC at pH greater than 6.5. Isoforms PSM-4 and PSM-5 would appear to
CC be physiologically irrelevant. Involved in prostate tumor
CC progression.
CC
CC -1- FUNCTION: Also exhibits a dipeptidyl-peptidase IV type activity.
CC In vitro, cleaves gly-Pro-AMC.
CC
CC -1- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
CC glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
CC
CC -1- COFACTOR: Zinc; Binds two ions per subunit. Required for NALADase
CC activity.
CC
CC -1- ENZYME REGULATION: The NALADase activity is inhibited by beta-
CC NAAG, quisqualic acid, 2-(phosphonomethyl) pentanedioic acid
CC (PMPA) and EDTA. Activated by cobalt.
CC
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Plasma membrane.
CC The PSMA isoform is cytoplasmic.
CC
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC
CC Name=PSMA-1;
CC IsoId=Q04609-1; Sequence=Displayed;
CC
CC Name=PSMA-2;
CC IsoId=Q04609-2; Sequence=VSP_005341;
CC
CC Name=PSMA-3;
CC IsoId=Q04609-3; Sequence=VSP_005342;
CC
CC Name=PSMA-4;
CC IsoId=Q04609-4; Sequence=VSP_005339, VSP_005340;
CC
CC Name=PSMA-5;
CC IsoId=Q04609-5; Sequence=VSP_005337, VSP_005338;
CC
CC Name=PSMA';
CC
CC -1- ISOId=Q04609-6; Sequence=VSP_005336;
CC
CC -1- TISSUE SPECIFICITY: Highly expressed in prostate epithelium. Also
CC expressed, in the small intestine, brain, kidney, liver, spleen,
CC colon and the capillary endothelium of a variety of tumors.
CC Expressed specifically in jejunum brush border membranes. In the
CC brain, highly expressed in the ventral striatum and brain stem. In
CC the prostate, the PSMA' cytosolic isoform is the most abundant
CC form in normal tissue, the membrane-bound PSMA-1 form in primary
CC prostate tumors. The PSMA-2 isoform also found in normal prostate
CC as well as in brain and liver.
CC
CC -1- INDUCTION: In the prostate, up-regulated in response to androgen
CC deprivation.
CC
CC -1- DOMAIN: The NALADase activity is found in the central region, the
CC dipeptidyl peptidase IV type activity in the C-terminal.
CC
CC -1- PTM: The first two amino acids at the N-terminus of isoform PSMA'
CC appear to be cleaved by limited proteolysis.
CC
CC -1- PTM: The N-terminus is blocked.
CC
CC -1- DISEASE: Defects in FOLH1 may be a cause of hyperhomocysteinemia
CC (HHC), a condition associated with increased risk of
CC cardiovascular disease, neural tube defects, and cognitive
CC deficits.
CC
CC -1- MISCELLANEOUS: PSMA is used as a diagnostic and prognostic
CC indicator of prostate cancer, and as a possible marker for various
CC neurological disorders such as schizophrenia, Alzheimer's disease
CC and Huntington's disease.
CC
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL: M99487; AAA60209.1; -
DR EMBL: S76978; AAB33750.2; -
DR EMBL: AF007344; AAC83972.1; -

	Query Match	98.2%	Score 2288:	DB 1	Length 750;	
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OY	61 DRYVILGGHRDSWFFGGIDPOSGAAVHEIYRSFGCTLKEGMRRPRTLLFASMDAEEFGL	120				
Dd	369 DRYVILGGHRDSWFFGGIDPOSGAAVHEIYRSFGCTLKEGMRRPRTLLFASMDAEEFGL	428				
OY	121 LGSTEWADNSRRLLOERGVAYINADSSIEGNTLTVDCTPLMTSLVYNTREKLSPDDEG	180				
Dd	429 LGSTEWAEENSRLLOERGVAVIYNADSSIEGNTLTVDCTPLMTSLVHNLTREKLSPDDEG	488				
OY	181 EKSLSYESWTKKSPSPERFSGMPRIKSLGSDNFEVFQRLGIASGRARYTNKMEETNKESG	240				
Dd	489 EKSLSYESWTKKSPSPERFSGMPRIKSLGSDNFEVFQRLGIASGRARYTNKMEETNKESG	548				
OY	241 YPLYHSVYETELYEKFYDPMEKHLYIAQYRGVAFELANSIVLPFCRDYAAYVLKRKYA	300				
Dd	549 YPLYHSVYETELYEKFYDPMEKHLYIAQYRGVAFELANSIVLPFCRDYAAYVLKRKYA	608				
OY	301 DKIVNISKKHQEKKTSYLSFDSLFAKNFTLEISKSESERLODEDKSNPIYLKMMNQOL	360				
Dd	609 DKIVSISKKHQEKKTSYVSFDSLFAKNFTLEISKSESERLODEDKSNPIYLKMMNDOL	668				
OY	361 MELTERAFIDPLGLDPDRPEYRHVIYAPSSHNKYAGESPFIYDALFDIESKDVPKRAMGY	420				
Dd	669 MELTERAFIDPLGLDPDRPEYRHVIYAPSSHNKYAGESPFIYDALFDIESKVDPKRAMGEV	728				
OY	421 KROITSVAFTVOAAETLSEVA 442					
Dd	729 KRQITVAAFIVQAALTELSEVA 750					

RESULT 2
FOHL_PIG STANDARD: PRT: 751 AA.

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AC      077564;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Glutamate carboxypeptidase II (EC 3.4.17.21) (membrane glutamate
DE      carboxypeptidase) (mCCP) (N-acetylated-alpha-linked acidic dipeptidase
DE      I) (NAALPase I) (Pteroylpoly-gamma-glutamate carboxypeptidase)
DE      (Poly(poly-gamma-glutamate carboxypeptidase) (PCGP) (Polate hydrolase
DE      1) (Prostate-specific membrane antigen homolog).
GN      FOHL OR NAALADI.
OS      Sus scrofa (pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxId=9823;
[1]
RN      RP SEQUENCE FROM N.A., AND SEQUENCE OF 200-210 AND 471-483.
RC      TISSUE=jejunal mucosa;
RX      MEDLINE=96852082; PubMed=9685395;
RA      Halsted C.H., Ling E.-H., Luthi-Carter R., Villanueva J.A.,
RA      Gardner J.M., Coyle J.T.;
RL      J. Biol. Chem. 275:30746-30746(2000).
RN      [3]
RP CHARACTERIZATION.
RX      MEDLINE=86089396; PubMed=2867095;

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[illegible]

Query Match 91.3%; Score 2126; DB 1; Length 751;
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61 DRYVILGHRDMSWFGIDPQSGAAVYETVRSFGTLKKGMRPRRTILFASMDAEFGL 120
|||||
370 DRYVILGHRDMSWFGIDPQSGAAVYETVRSFGTLKKGMRPRRTILFASMDAEFGL 429
121 LGSTWAEADNSRLQERGVAYINADSSIEGNYTLRVDCPTPLMSLVNLTKEKSPDEGF 180
|||||
430 FGSTWAEADNSRLQERGVAYINADSSIEGNYTLRVDCPTPLMSLVNLTKEKSPDEGF 489
181 EGSGLYESWTKKSPSPFSGMPRTSKLGSNDPEVFQRLGASGRARYTNWENKPSG 240
|||||
490 EGSGLYESWTKKSPSPFSGMPRTSKLGSNDPEVFQRLGASGRARYTNWENKPSG 549
241 YPLHSVYETELVEKEKYDPMFKYHLTAQYRGGMVELANSIYLPDPCRDYAVVLRKYA 300
550 YPLHSVYETELVEKEKYDPMFKYHLTAQYRGGMVELANSIYLPDPCRDYAVVLRKYA 609
301 DKYVNSMKHPQEMKTYSLSFDSLPSAVKNFTETLASKFSERLQDFDKSNPILRLMNDOL 360
610 DKYVNSMKHPQEMKTYSLSFDSLPSAVKNFTETLASKFSERLQDFDKSNPILRLMNDOL 669
361 MELERAFDPLGLDPRPYRHVYAPSSHNKYAGESPFGIYDALFDIESKYPDKAMGW 420
670 MELERAFDPLGLDPRPYRHVYAPSSHNKYAGESPFGIYDALFDIESKYPDKAMGW 729
421 KROISIAFTYQAAAGTIREVA 442
730 KROISIAFTYQAAAGTIREVA 751

RESULT 3
FOHL_RAT STANDARD: PRT; 752 AA.

AC P70627;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
DE Glutamate carboxypeptidase II (EC 3.4.17.21) (Membrane glutamate
carboxypeptidase) (MGCPI) (N-acetylated-alpha-linked acidic dipeptidase
I) (NAALADase I) (Pteroylpolymy-gamma-glutamate carboxypeptidase)
DE (Folypoly-gamma-glutamate carboxypeptidase) (FGCP) (Folate hydrolase
I) (Prostate-specific membrane antigen homolog).
DE FOLH1 OR NAALAD1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_Taxid=10116;
[1]
SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Hippocampus;
RA MEDLINE=98041505; PubMed=9375657;
Bzdega T., Turli T., Wroblewska B., She D., Chung H.S., Kim H.,
Neale J.H.;
"Molecular cloning of a peptidase against N-acetylaspartylglutamate
from a rat hippocampal cDNA library."
J. Neurochem. 69:2270-2277(1997).
[2]
SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley; TISSUE=Brain;
RA MEDLINE=98169524; PubMed=9501243;
Luthi-Carter R., Berger U.V., Barczak A.K., Enna M., Coyle J.T.;
"Isolation and expression of a rat brain cDNA encoding glutamate
carboxypeptidase II."
Proc. Natl. Acad. Sci. U.S.A. 95:3215-3220(1998).
[3]

RP SEQUENCE OF 284-752 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98149377; PubMed=8570628;
RA Carter R.E., Feldman A.R., Coyle J.T.;
RT "Prostate-specific membrane antigen is a hydrolyase with substrate and
pharmacologic characteristics of a neuroleptidase."
Proc. Natl. Acad. Sci. U.S.A. 93:749-753(1996).
[4]
RP SEQUENCE OF 284-752 FROM N.A.
RC TISSUE=Brain;
RA Luthi-Carter R., Berger U.V., Barczak A.K., Enna M., Coyle J.T.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
[5]
RP ALTERNATIVE SPLICING.
RA Bzdega T., Turli T., Wroblewska B., Neale J.H.;
RT "Molecular cloning of alternatively spliced variants of the peptidase
against N-acetylaspartylglutamate (NAAG) from human and rat nervous
systems."
Abstr. Soc. Neurosci. 24:579-579(1998).
-1- FUNCTION: Has both folate hydrolase and N-acetylated-alpha-linked-
acidic dipeptidase (NAALADase) activity. Has a preference for tri-
alpha-glutamate peptides (By similarity). In the intestine,
required for the uptake of folate. In the brain, modulates
excitatory neurotransmission through the hydrolysis of the
neuropeptide, N-acetylaspartylglutamate (NAAG), thereby releasing
glutamate.
-1- FUNCTION: Also exhibits a dipeptidyl-peptidase IV type activity
(By similarity). In vitro, cleaves Gly-Pro-Awk (By similarity).
-1- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
-1- COFACTOR: Zinc; Binds two ions per subunit. Required for NAALADase
activity.
-1- ENZYME REGULATION: The NAALADase activity is inhibited by beta-
NAG, quasilic acid and 2-(phosphonomethyl)glutaric acid (PMG).
-1- SUBCELLULAR LOCATION: Type II membrane protein. Plasma membrane
(By similarity).
-1- ALTERNATIVE PRODUCTS:
Event-Alternative splicing: Named isoforms=3;
Comment-Experimental confirmation may be lacking for some
isoforms;
Name=1;
IsoId=P70627-1; Sequence=Displayed;
Name=2; Synonyms=Short form;
IsoId=P70627-2; Sequence=Not described;
Name=3; Synonyms=Long form;
Note=Probably inactive;
Name=3; Synonyms=Long form;
IsoId=P70627-3; Sequence=Not described;
-1- TISSUE SPECIFICITY: Widely expressed throughout brain regions with
highest levels in the hippocampus, dentate gyrus, piriform cortex,
choroid plexus of ventricles, pineal gland, anterior lobe of the
pituitary gland and supraoptic nucleus. High levels also found in
the cerebral cortex, substantia nigra, pontine nucleus and the
granule cell layer of cerebellum. Highly expressed in astrocytes
and non-myelinating Schwann cells. Also expressed in kidney,
localizing to the proximal brush border of the renal tube.
-1- DOMAIN: The NAALADase activity is found in the central region, the
dipeptidyl peptidase IV type activity in the C-terminal.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.

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EMBL: U75973; AAC53423.1;
EMBL: AF040256; AAC40067.1;
EMBL: AF039707; AAB96759.1;
MEROPS: M28.010;
InterPro: IPR003137; PA.
Pfam: PF02225; PA. 1.

ON NALAD2 Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MBLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinaigawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batool S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Peele G., Quackenbush J.,
 RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein L.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamila M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyshniewski B., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 CC -I- FUNCTION: Has N-acetylated-alpha-linked-acidic dipeptidase
 CC (NALADase) activity (By similarity). Also exhibits a dipeptidyl-
 CC peptidase IV type activity. In vitro, cleaves Gly-Pro-AMC (By
 CC similarity).
 CC -I- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
 CC glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
 CC -I- COFACTOR: Zinc. Binds two ions per subunit. Required for NALADase
 CC activity (By similarity).
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -I- DOMAIN: The NALADase activity is found in the central region, the
 CC dipeptidyl peptidase IV type activity in the C-terminal.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
 CC
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 CC
 DR EMBL: AK012270; BAB28132.1; -
 DR MEROPS: M28.012; -
 DR MGD: MGI:1919810; Nalad2.
 DR Pfam: PF04389; Peptidase_M28; 1.
 DR Pfam: PF04253; TFR_dimer; 1.
 DR Hydrolase: Carboxypeptidase; Metalloprotease; Zinc; Aminopeptidase;
 KW Dipeptidase; Serine protease; Transmembrane; Glycoprotein;
 KW Signal-anchor; Multifunctional enzyme.
 FT NON_TER 1
 FT DOMAIN 1
 FT ACT_SITE 135 94 NALADASE.
 FT ACT_SITE 173 173 CHANGE RELAY SYSTEM (POTENTIAL).
 FT ACT_SITE 196 196 CHARGE RELAY SYSTEM (POTENTIAL).
 FT METAL 60 60 ZINC 1 (BY SIMILARITY).
 FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 257 AA; 29081 MW; 1E90769095E50BA CRC64;
 Query Match 39.3%; Score 916; DB 1; Length 257;
 Best Local Similarity 66.5%; Pred. No. 5,2e-61;
 Matches 167; Conservative 43; Mismatches 41; Indels 0; Gaps 0;

DE Ileum brush border membrane protein (I1100).
 GN MALADL OR MALADASEL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7 AND 8).
 RC TISSUE=Small Intestine;
 RX MEDLINE=99185063; PubMed=10085079;
 RA Pangalos M.N., Neefs J.-M., Somers M., Verhasselt P., Bekkers M.,
 RA van der Helm L., Fraipont E., Ashton D., Gordon R.D.,
 RT "Isolation and expression of novel human glutamate carboxypeptidases
 RT with N-acetylated alpha-linked acidic dipeptidase and dipeptidyl
 RT peptidase IV activity".
 RT J. Biol. Chem. 274:8470-8483(1999).
 RL [2]
 RP SEQUENCE OF 419-740 FROM N.A.
 RC TISSUE=Ileum;
 RX MEDLINE=98049571; PubMed=9388249;
 RA Shneider B.L., Thevananthar S., Moyer M.S., Walters H.C., Rinaldo P.,
 RA Devarajan P., Sun A.Q., Dawson P.A., Anantharayanan M.;
 RT "Cloning and characterization of a novel peptidase from rat and human
 RT ileum".
 RL J. Biol. Chem. 272:31006-31015(1997).
 CC -1- FUNCTION: MALADASE-like activity unknown. Has no NAAG hydrolyzing
 CC activity. Exhibits a dipeptidyl-peptidase IV type activity. In
 CC vitro, cleaves Gly-Pro-AMC (By similarity).
 CC -1- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
 CC glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
 CC -1- COFACTOR: Zinc. Binds two ions per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Ileal brush border
 CC membrane.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=8;
 CC Name=1;
 CC IsoId=Q9U0Q1-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9U0Q1-2; Sequence=VSP_005343;
 CC Name=3;
 CC IsoId=Q9U0Q1-3; Sequence=VSP_005344;
 CC Name=4;
 CC IsoId=Q9U0Q1-4; Sequence=VSP_005345;
 CC Name=5;
 CC IsoId=Q9U0Q1-5; Sequence=VSP_005346, VSP_005347;
 CC Name=6;
 CC IsoId=Q9U0Q1-6; Sequence=VSP_005348, VSP_005349;
 CC Name=7;
 CC IsoId=Q9U0Q1-7; Sequence=VSP_005350, VSP_005351;
 CC Name=8;
 CC IsoId=Q9U0Q1-8; Sequence=VSP_005352, VSP_005353;
 CC -1- TISSUE SPECIFICITY: Mainly expressed in the distal small
 CC intestine. Also expressed in the spleen and testis. Weak
 CC expression in the brain, locating mainly to the brain stem,
 CC amygdala, thalamus and ventral striatum. Isoforms 2 and 3 are
 CC found in the small intestine and colon.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
 CC -----
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 CC -----
 CC EMBL: AJ012371; CAB39968.1; -;
 CC EMBL: AF010141; AAB87645.1; -;
 CC MEROPS: M28. 011. -;
 CC MIM: 602640. -;
 CC InterPro: IPR003137; PA.
 CC Pfam: PF02225; PA; 1.
 CC Pfam: PF04389; Peptidase_M28; 1.

	FT	Pfam: PF04253; TPR dimer: 1.
KM	Hidrolase; Carboxypeptidase; Metalloprotease; Zinc: Aminopeptidase;	
KW	Dipeptidase; Serine protease; Transmembrane; Glycoprotein;	
KW	Signal-anchor; Multifunctional enzyme; Alternative splicing.	
FT	DOMAIN 1 6 CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 7 28 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).	
FT	DOMAIN 29 740 EXTRACELLULAR (POTENTIAL).	
FT	NADLADASE.	
FT	ACT_SITE 263 379 NOCTLOPHILE (NADLADASE) (BY SIMILARITY).	
FT	ACT_SITE 416 416 CHARGE RELAY SYSTEM (POTENTIAL).	
FT	ACT_SITE 617 617 CHARGE RELAY SYSTEM (POTENTIAL).	
FT	ACT_SITE 657 657 CHARGE RELAY SYSTEM (POTENTIAL).	
FT	METAL 687 687 ZINC 2 (BY SIMILARITY).	
FT	METAL 368 368 ZINC 1 AND 2 (BY SIMILARITY).	
FT	METAL 378 378 ZINC 1 (BY SIMILARITY).	
FT	METAL 417 417 ZINC 2 (BY SIMILARITY).	
FT	METAL 445 445 ZINC 1 (BY SIMILARITY).	
FT	METAL 545 545 ZINC 1 (BY SIMILARITY).	
FT	CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 492 492 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	VARSPLIC 161 201 Missing (in isoform 2).	
FT	VARSPLIC 296 330 /FTid=VSP_005343.	
FT	VARSPLIC 359 359 Missing (in isoform 3).	
FT	VARSPLIC 502 522 /FTid=VSP_005344.	
FT	VARSPLIC 523 740 PSLGSLGAGSDYAPVHVLGI -> PRLQPSGGPDSECC DSPAQ (in isoform 5).	
FT	VARSPLIC 502 543 Missing (in isoform 6).	
FT	VARSPLIC 544 740 /FTid=VSP_005345.	
FT	VARSPLIC 562 579 PSLGSLGAGSDYAPVHVLGI -> PRLQPSGGPDSECC DSPAQ (in isoform 5).	
FT	VARSPLIC 580 740 /FTid=VSP_005346.	
FT	VARSPLIC 619 635 Missing (in isoform 7).	
FT	VARSPLIC 636 740 /FTid=VSP_005347.	
FT	VARSPLIC 420 424 PSLGSLGAGSDYAPVHVLGI -> PRLQPSGGPDSECC DSPAQ (in isoform 5).	
FT	SEQUENCE 740 AA; 80620 MW; EZE5AAC9E5056A14 CRC64; Missing (in isoform 6).	
Query Match	Best Local Similarity 37.1%; Score 863.5; DB 1; Length 740;	
Matches 185; Conservative 91; Mismatches 146; Indels 39; Gaps 13	Pred. No. 1.7e-56; Query Match	
OY	1 MGGSAPPDDSSMRGSLKSTVYNGPGF--TGNF-STOKYKMHISTNEVTRLYNVIGTLRGA 57	
Db	298 LNETLAP-ATWGALGCHRYLRGPGRDPDGPPADSVGVNSVLELRNSSNLVIITIRGA 356	
OY	58 VEPDRRVIIIGHRDSWVGIDPOSGAAVVEIYVRSGTLKKES-WMPRTTILFAAMDAE 116	
Db	357 VEPDRIVYLGNHRDSWVGADVPSSGTIVLLELSRGITLTKKTGMTPRRSIFYASMGAE 416	
OY	117 EFELGSTMEADNRLLQERGAVALINDSSIENSYTLRDVCPLMYSLVYNLTKEIKSP 176	
Db	417 EPELLISIEFEETEFENKLQERTVAIYNVDISVANATIRVQGTPRPVQSVFSAIKELRSR 476	
OY	177 DEGEFKSLYESWTK--NSPSPFSFGMRISKLSGNDVEVFQRGLIASGARVYTKNME 234	

Db 477 GPG--DUSTDNMTRREYRNRSSPVGLVPSGLSLAGSDYAPFVHFLGISMDIAYT--YD 532
QY 235 TNKFSG--YPLLYHSVYETLVEKEFYDPMFKYHLTVAOVRCGMVFEELANSIVLPEDCDRY 292
Db 533 RSKTSARHLYPHYHAFDLPFDYDKFDLPDGFSGHQAIVATAGSVILRLSDSFLLKXSDY 592
QY 293 AVVLRKADKLYINSMKHPD-----MKYVSLSPDLSFAVKNFTETASKFESRLQDFDK 347
Db 593 SETLRSE-----LQAAQODLGCALLEOHSISLGPVLTAAVEKEFAEAAALGGRISTLOK 644
QY 348 S--PILLRMNDOLMFLERAFIDPLGDPREFRYHYAPS-----SHNKYAGSPFCIY 401
Db 645 GSPPLQVRLMNDOLMLERFTLNPRAPEERYSHVLMAPSHELGRSH-----IPGLS 697
QY 402 DALFDIESKVDPSKMGDVYKROISVAAFVQAAAEITLSEVA 442
Db 698 NACSRARDTASGSEAWAEVQROSLIVTALGGAATLRPA 738
RESULT 9
GCP2_CAEEL STANDARD; PRT; 751 AA.
AC P91406:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate carboxypeptidase II homolog (EC 3.4.17.21).
GN R57.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2.
RA Favello A., Rifkin L., Chlapelli B.:
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Release of an unsubstituted, C-terminal
CC glutamyl residue, typically from Ac-Asp-Glu or pteroyl-gamma.
CC -1- COFACTOR: zinc; Binds two ions per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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CC -----
CC EMBL; U88179; AAB52660.1; -.
CC PIR: T30154; T30154.
DR MEROPS; M28.010; -.
DR WormPep; R57.1; CE12844.
DR InterPro; IPR001317; PA.
DR Pfam; PF02225; PA; 1.
DR Pfam; PF04389; Peptidase_M28; 1.
DR Pfam; PF04253; TFR_dimer; 1.
DR Hypothetical protein; Hydrolase; Carboxypeptidase; Metalloprotease;
KW Zinc; Transmembrane; Glycoprotein; Signal-anchor.
KW DOMAIN 1
RN TRANSMEM 7 23
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT CATALYTIC (BY SIMILARITY).
FT NUCLEOPHILE (BY SIMILARITY).
FT ZINC 2 (BY SIMILARITY).
FT ZINC 1 AND 2 (BY SIMILARITY).
FT ZINC 1 (BY SIMILARITY).
FT ZINC 2 (BY SIMILARITY).
FT ZINC 1 (BY SIMILARITY).
FT METAL 543 543
FT METAL 543 543

FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 532 532 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 587 587 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 751 AA; 83683 MW; 1A08AA4974FA29C7 CRC64;
Query Match 27.1%; Score 631.5; DB: 1; Length 751;
Best Local Similarity 32.8%; Pred. No. 2.9e-39;
Matches 151; Conservative 101; Mismatches 168; Indels 41; Gaps 20;
QY 6 PDDSSWNGSGSL--KRYVNWGPGFTNGFNSTOKYKMHHSSTNEVTRYNYIGTLRGAVEEDRY 63
Db 306 PAPSDMOGFVQGNLTLYLGRGFVNG---EKLSIVHSELTKRIKRWYIGYIRGSEEDSY 362
QY 64 VILGHRDQWVFGGIDPQSGAAVYHETRS--FGLTKRGRMPRTTLFASMDAEEFGILG 122
Db 363 IMLGNHFDAMWYGSIDPNSGTAVALAEVARAMQGTINETSMPATIVFNAMDADEEFLIG 422
QY 123 STEWAE DNSRLDERGVAIYNADSSIEGNTTLKYDCTPLMYSLVYNTLTKELKSPD--EGF 180
Db 423 STEVEEFVNILQRAVYIYIMD-CIOGNISLHVDPILEHVAIEASKQVENSRRERS 481
QY 181 EG-KSIESTMKRSPESEFGMPRIKSGNDPEVEFGQGLIASGARAT-KWMTNKF 238
Db 482 RGRKTLTYDMWKVFPDKK-AGVPRIVPGGSDHAPLANRQVIV--INTEFNKYYT--W 536
QY 239 SGYPLYSVYET-YELVEKEFYDPMFKYHLTVAOVRCGMVFEELANSIVLPEDCDRYA-VVL 296
Db 537 DTYPLHYHMYETPEPSNHLDTDNLVSKAIGQYWAELATFPDDVDTLPNNTJHFAFSVML 596
QY 297 RKYADKI-----YINSMKHPQEMKT-YSLSPDLSFAVKNFTETASKFESERL----QDF 345
Db 597 KYLPQLKTTIGSLINVSRSDFEDIRTOYAL----LSKSAODLLTMSKKFQETIHFTQHSF 652
QY 346 DKS--NPILLRMNDOLMFLERAFIDPLGDPREFRYHYAPSINNKYAGSPFCIYD 402
Db 653 SQNPYDKHNAVNAVERKSKTERCFINRGVSMANPSARHLYFSVSDSYSSSLMAGVON 712
QY 403 AL--FDIESKVDPSKMGDVYKROISVAAFVQAAAEITLSEV 441
Db 713 AINSYDLN---PTKKGRLREINQISIVQVIGVNTLRDV 750
RESULT 10
GCP2_ARATH STANDARD; PRT; 705 AA.
AC O9M158;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable glutamate carboxypeptidase II (EC 3.4.17.21).
GN AMP1 OR AT3G54720 OR T5N23.80.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta; TISSUE-Siliques;
RX MEDLINE-21434423; Pubmed-11549767;
RA Hellmell C.A., Chin-Atkins A.N., Wilson I.W., Chapple R.,
RA Dennis E.S., Chaudhury A.:
RT "The Arabidopsis AMP1 gene encodes a putative glutamate
RT carboxypeptidase.";
RL Plant Cell 13:2115-2125(2001).
RN [2]
RP SEQUENCE FROM N.A.

Gloeckner G., Scherer S., Schatevov R., Boright A.P., Weber J.,
RA Tsui L.-C., Rosenthal A.,
RA "Large-scale sequencing of two regions in human chromosome 7q22:
RT analysis of 650 kb of genomic sequence around the EPO and CMT1A loci
RT reveals 17 genes.";
RL Genome Res. 8:1060-1073(1998).
RN [3]
RP SEQUENCE OF 1-158 AND 370-801 FROM N.A.
RC TISSUE-Carlinome, and Embryo;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,
RA Watanabe S., Chiba Y., Ishida S., Murakami K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,
RA Ninomiya K., Iwayanagi T.,
RT "NEO human cDNA sequencing project.";
RT Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP DISEASE.
RX MEDLINE-20264357; PubMed-10802645; De Gobbi M., Garozzo G.,
RA Camaschella C., Roetto A., Cali A., Gasparini P.,
RA Carella M., Majorano N., Totaro A., Gasparini P.,
RT "The gene TFR2 is mutated in a new type of haemochromatosis mapping to
RT 7q22.";
RT Nat. Genet. 25:14-15(2000).
RN [5]
RP VARIANT HFE3 LYS-172.
RX MEDLINE-21133241; PubMed-11313241;
RA Roetto A., Totaro A., Piperno A., Piga A., Longo F., Garozzo G.,
RA Cali A., De Gobbi M., Gasparini P., Camaschella C.,
RT "New mutations inactivating transferrin 2 in hemochromatosis type
RT 3.";
RT Blood 97:2555-2560(2001).
RL -1- FUNCTION: Mediates cellular uptake of transferrin-bound iron in a
non-iron dependent manner. May be involved in iron metabolism,
hepatocyte function and erythrocyte differentiation.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. The beta isoform
lacks the transmembrane domain and is probably intracellular.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name-Alpha:
CC IsoId-Q90P52-1; Sequence-Displayed;
CC Name-Beta:
CC IsoId-Q90P52-2; Sequence-VSP_005354;
CC Name-Gamma:
CC IsoId-Q90P52-3; Sequence-VSP_005355;
CC -1- TISSUE SPECIFICITY: Predominantly expressed in liver. While the
alpha form is also expressed in spleen, lung, muscle, prostate and
peripheral blood mononuclear cells, the beta form is expressed in
all tissues tested, albeit weakly.
CC -1- DISEASE: Defects in TFR2 are a cause of hereditary hemochromatosis
type 3 (HFE3) [MIM:604250]. HFE3 is a disorder of iron homeostasis
resulting in iron overload and has a phenotype indistinguishable
from that of hereditary hemochromatosis (HH). HH is characterized
by abnormal intestinal iron absorption and progressive increase of
total body iron, which results in midlife in clinical
complications including cirrhosis, cardiopathy, diabetes,
endocrine dysfunctions, arthropathy, and susceptibility to liver
cancer. Since the disease complications can be effectively
prevented by regular phlebotomies, early diagnosis is most
important to provide a normal life expectancy to the affected
subjects.
CC -1- MISCELLANEOUS: The variant lys-172 found in hereditary
hemochromatosis type III affects the putative initiation codon of
the beta isoform thus preventing its translation.
CC -1- SIMILARITY: BELONGS TO PERIDASE FAMILY M28B.
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF067864; AAD45561.1; -
CC DR EMBL: AF053356; AAC78796.1; -
CC DR EMBL: AK022002; BAB13951.1; -
CC DR EMBL: AK000421; BAA91153.1; ALT_INIT.
CC DR HSSP: P02786; ICX8.
CC DR MEROPS: M28.973; -
CC DR GeneW: HGNC:11762; TFR2.
CC DR MIM: 604250; -
CC DR GO: 0005887; C: integral to plasma membrane; NAS.
CC DR GO: 0004998; F: transferrin receptor activity; NAS.
CC DR GO: 0006826; P: iron ion transport; NAS.
CC DR InterPro: IPR003137; PA.
CC DR Pfam: PF02225; PA; 1.
CC DR Pfam: PF04389; Peptidase_M28; 1.
CC DR Pfam: PF04253; TFR_dimer; 1.
CC KW Transmembrane; Glycoprotein; Receptor; Signal-anchor;
KW Alternative splicing; Disease mutation.
KW DOMAIN 1 83 CYTOPLASMIC (POTENTIAL).
KW TRANSMEM 84 104 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
KW TRANSME 1 83
FT DOMAIN 105 801
FT SITE 23 26
FT DISULFID 108 108
FT DISULFID 111 111
FT CARBOHYD 240 240
FT CARBOHYD 339 339
FT CARBOHYD 540 540
FT CARBOHYD 754 754
FT VARSPPLIC 1 171
FT VARSPPLIC 343 369
FT VARSPPLIC 172 172
FT VARIANT 172 172
FT CONFLICT 712 712 R -> R1PLSAOV (IN REF. 2).
FT SEQUENCE 801 AA; 88755 MW; D3D3082BA85413A CRC64;
SO
Query Match 19.9%; Score 462.5; DB 1; Length 801;
Best Local Similarity 27.4%; Pred. No. 1.1e-26;
Matches 124; Conservative 93; Mismatches 188; Indels 47; Gaps 12;
QY 2 GGSAPDSSWRGSLKYS-YVGGPFTGNFSTQYVKHHIHSNTEVRYNYIGLRGAVEP 60
DB 373 GPVAPGE--WQSGILSGPYHLGP-----PRLRLVNNHRTSTPINNIFGCIKGRSEP 423
QY 61 DRYVILGHRDQSWFGIDPQGAAYVHETVRSFGTLKKGWPRRTILRASMDAEEFGL 120
DB 424 DHYVITAQRDAWPGAKSAVGTAILLELVRTSSVWSNGFRRLSLFISMDCGDFGS 483
QY 121 LGSFTEAEDNSRLLOERGVAVINADSSIEGNYTLRVDCITPLMSLYVNLKELKSPDEGF 180
DB 484 VGSFTEMLEGYSLVHLAAVYVSLDNAVLGDKRPHAKTSPILSLISLVKQVDSPNH-- 541
QY 181 EGKSLYESWTWKSPSPERSGMPRIKSLGSGNDFEVPFQRIAGGRARYTNWETNFKFSG 240
DB 542 SGQRLTEQVNTNSMWAELVIRPLPMDSSAVSFYAF--GVPPVERVSFMEDDQ-----A 593
QY 241 YPLIHSVETEELVEKEFDPNF-KYHLFVAQVRGAWFELANSIVLPEDCDVAIVLKKY 299
DB 594 YPFLTKEDTYENLKVLOGRLPAVAQAVADLAQOLLIRLSDLLPLDFRGYDVAFLRH 653
QY 300 ADKIYNISMKRPOEKKYSLSFDSIFSAVKNFTETASKFSERLQDFDKSNPILRLRMNDQ 359
DB 654 IGNLNEFS-----GDIKAGILQLQWYISARGDYIRAAEKLROEIVYSSEERDERLTRMYNVR 709
QY 360 IMFLERAFIDPLGLP-DRPYTRHYIYAPSSHNKYA-----GSPFHYIDALPDI 407
DB 710 IMRVEFVFLSQVSPADSPF-RHIFMGKGDHTIGLDDLRLRLRSNSGCTGQATISSTGFO 768

QY 408 ESKVDPKAMGVKROISVAFAFVQAAETLS 439
 DB 769 ESR-----FRRLALTWTTCGCAANALS 791

RESULT 12
 TFR2_MOUSE
 ID TFR2_MOUSE STANDARD: PRT: 798 AA.
 RC 09JRKX3: 092016: 099M09: 09CPT2:
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 GN Transferin receptor protein 2 (TFR2).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A. (ISOFORM 1).
 RP TISSUE-Embryo:
 RX MEDLINE=20160931; PubMed=10681454;
 RA Fleming R.E., Migas M.C., Holden C.C., Mahood A., Britton R.S.,
 RA Tomatsu S., Bacon B.R., Sly W.S.;
 RT "Transferrin receptor 2: Continued expression in mouse liver in the
 RT face of iron overload and in hereditary hemochromatosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2214-2219(2000).
 RN [2]
 RC SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RP TISSUE-Erythrocytopenia;
 RX MEDLINE=21426540; PubMed=11535534;
 RA Kawabata H., Germain R.S., Ikezoe T., Tong X., Green E.M.,
 RA Gombart A.F., Koefler H.P.;
 RT "Regulation of expression of murine transferrin receptor 2.";
 RL Blood 98:1949-1954(2001).
 RN [3]
 RC SEQUENCE FROM N.A. (ISOFORM 1).
 RP STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
 RA Morone P., Rung B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [4]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=23388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stalcheva M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Smerchek A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RC SEQUENCE OF 1-278 FROM N.A.
 RP STRAIN=129/SV;
 RX MEDLINE=21138439; PubMed=11239002;
 RA Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsai L.-C.,
 RA Miller W., Koop B.F.;
 RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human
 RT chromosome 7q22 with the orthologous region on mouse chromosome 5.";
 RL Nucleic Acids Res. 29:1352-1365(2001).
 CC -1- FUNCTION: Mediates cellular uptake of transferrin-bound iron in a
 CC non-iron dependent manner. May be involved in iron metabolism,
 CC hepatocyte function and erythrocyte differentiation.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Isoform 3 may be
 CC cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-3;
 CC Name=1;
 CC IsoId=Q9JRKX3-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9JRKX3-2; Sequence=VSP_005357; VSP_005358;
 CC Note=lacks most of the extracellular domain. No experimental
 CC confirmation available;
 CC Name=3;
 CC IsoId=Q9JRKX3-3; Sequence=VSP_005356;
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in liver. Also
 CC expressed in kidney, spleen, brain, lung, heart and muscle with
 CC very low expression in kidney, muscle and heart.
 CC -1- DEVELOPMENTAL STAGE: First expressed between embryo days 8 and 11.
 CC In the liver, expression increases during development from embryo
 CC day 13 to adulthood while, in the spleen, levels remain constant
 CC throughout development.
 CC -1- INDUCTION: Down-regulated during erythrocyte differentiation.
 CC Expression unchanged by cellular iron status.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
 CC
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 CC
 CC EMBL; AF222895; AAF37272.1; -
 CC EMBL; AF207741; AAL05976.1; -
 CC EMBL; AF207742; AAL05977.1; -
 CC EMBL; AK004965; BAB23705.1; -
 CC EMBL; AK004848; BAB23614.1; -
 CC EMBL; BC013654; AAH13654.1; -
 CC EMBL; AF312033; AAK28830.1; -
 CC HSSP; P02786; 1CX8.
 CC MGD; MGI:1354956; Tfr2.
 CC InterPro; IPR003137; PA.
 CC Pfam; PF02225; PA; 1.
 CC Pfam; PF04389; Peptidase_M28; 1.
 CC Pfam; PF04253; TFR_dimer; 1.
 CC Transmembrane; Glycoprotein; Receptor; Signal-anchor;
 CC Alternative splicing
 CC DOMAIN 1 81 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 82 102 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 FT

FT	DOMAIN	103	798	EXTRACELLULAR (POTENTIAL).
FT	SITE	23	26	ENDOCYTOSIS SIGNAL (POTENTIAL).
FT	DISULFID	106	106	INTERCHAIN (POTENTIAL).
FT	DISULFID	109	109	INTERCHAIN (POTENTIAL).
FT	CARBOHYD	235	235	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	334	334	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	535	535	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	12	93	Missing (in isoform 3).
FT	VARSPLIC	237	237	/FTId-VSP_005356.
FT	VARSPLIC	238	798	T -> TVRPPGMAHVLIG (in isoform 2).
FT	VARSPLIC	238	798	/FTId-VSP_005357.
FT	VARSPLIC	238	798	Missing (in isoform 2).
FT	FTId-VSP	005358		/FTId-VSP_005358.
FT	CONFLICT	25	25	R -> P (IN REF. 2; AF207742).
FT	CONFLICT	42	42	G -> V (IN REF. 2; AF207742 AND 5).
FT	CONFLICT	103	103	R -> P (IN REF. 2; AF207742).
FT	CONFLICT	151	151	T -> N (IN REF. 4).
FT	CONFLICT	248	248	S -> I (IN REF. 2).
FT	CONFLICT	287	287	A -> V (IN REF. 2).
FT	CONFLICT	595	595	K -> E (IN REF. 1).
SO	SEQUENCE	798 AA;	88402 MW;	FA616EE3FFZAA4 CRC64;
Query Match				
Best Local Similarity		19.6%; Score 457.5; DB 1; length 798;		
Matches 125; Conservative		27.4%; Pred. No. 2.6e-26;		
		92; Mismatches 185; Indels 55; Gaps 14;		

[illegible]

RP	SEQUENCE FROM N.A..
RC	TISSUE=Testis; PubMed=2126342;
RX	MEDLINE=91125359; G15012 M.D.;
RA	Roberts K.P., G15012 M.D.;
RT	"Characterization of rat transferrin receptor cDNA: the regulation of transferrin receptor mRNA in testes and in Sertoli cells in culture.",
RL	Mol. Endocrinol. 4:531-542(1990).
CC	-!- FUNCTION: Cellular uptake of iron occurs via receptor-mediated endocytosis of ligand-occupied transferrin receptor into specialized endosomes. Endosomal acidification leads to iron release. The apotransferrin-receptor complex is then recycled to the cell surface with a return to neutral pH and the concomitant loss of affinity of apotransferrin for its receptor. Transferrin receptor is necessary for development of erythrocytes and the nervous system (By similarity).
CC	-!- SUBUNIT: Homodimer; disulfide-linked. Binds one transferrin molecule per polypeptide chain (By similarity).
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
CC	-!- TISSUE SPECIFICITY: In testis, expressed in Sertoli cells, peritubular myoid cells and in germinal cells. Highest levels in Sertoli cells.
CC	-!- PTM: N- and O-glycosylated, phosphorylated and palmitoylated (By similarity).
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
CC	-----
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CC	-----
DR	EMBL; M58040; AAA42273.1; .
DR	PIR; A34549; A34549.
DR	HSSP; P02786; ICX8.
DR	InterPro: IPR003137; PA.
DR	Pfam; PF02225; PA.1.
DR	Pfam; PF04389; Peptidase_M28; 1.
DR	Pfam; PF04253; TFR_dimer; 1.
RW	Transmembrane; Glycoprotein; Receptor; Lipoprotein; Palmitate;
KW	Signal-anchor; Endocytosis; Phosphorylation.
FT	NON_TER 1
FT	DOMAIN 1
FT	SITE 431 622
FT	SITE 508 510
FT	CARBOHYD 109 109
FT	CARBOHYD 113 113
FT	CARBOHYD 179 179
FT	CARBOHYD 584 584
FT	CARBOHYD 589 589
SEQUENCE	622 AA; 70152 MW; 831EFC16DE55703 CRC64;

Query Match	19.1%	Score 445.5:	DB 1:	length 622:
Best Local Similarity	26.0%	Pred. 1.56-25:		
Matches	118:	Conservative	89:	Mismatches 180: Indels 67: Gaps 11:

OY	1	MGSAPP----	DSWSRSLKAVSYVGFGEFTGNSTÖKYKMHINSTEYTRIVYVIGL	56
		:-:-:-:-	:-:-:-:-	
Db	211	MEGACPSWMNDISCK--LELSQN-----	QWVKLVNNVLETRLNFYGIK	257
		:-:-:-:-	:-:-:-:-	
OY	57	AVEDPRVILIGHSDSWVFGIDPGSAAVVHETVRSFQ--TLKKEGMRPRTILFASMDA	115	
		:-:-:-:-	:-:-:-:-	
Db	258	YEEEDRIIVYGAQDANGPGYAKASVGTGLLKLIAQYFSDIMSKDGRPSISITFAWTA	317	
		:-:-:-:-	:-:-:-:-	
OY	116	EEFGCLLSTEMAEDNSRLLQERGVAVINADSSIEGNTTLRYDCTPLMYSLIVYNLTKEKLS	175	
		:-:-:-:-	:-:-:-:-	
Db	318	GDYGAVPPTLELIEGYSLLHKAFETYINLDRKVVLGTFNFRVYASAPLLTYLTMGKIMQDVKH	377	
		:-:-:-:-	:-:-:-:-	
OY	176	PDEGFEKRSILY--ESMWRKSPSPFEGSMPIRKSIGSNDPEVFQRLGISGRARYTKNN	233	
		:-:-:-:-	:-:-:-:-	
Db	378	P---IDGRYILRNSNMISK-----IEELSDNMAEPFLYASGIIPAVSCFCEED	422	
		:-:-:-:-	:-:-:-:-	
OY	234	ETNFESGPLYHSVETVELVEKEFYDMEFKYHLTLVAOGRGMVELANSLVLPFCDCRYA	293	
		:-:-:-:-	:-:-:-:-	

RN [2]
 RP SEQUENCE OF 25-301 FROM N.A.
 RC TISSUE=Myeloma;
 RX MEDLINE=85159078; PubMed=2984291;
 RA Stearne P.A., Pletersz G.A., Goding J.W.;
 RT "cDNA cloning of the murine transferrin receptor: sequence of trans-
 membrane and adjacent regions.";
 RL J. Immunol. 134:3474-3479(1985).
 RN [3]
 RP SEQUENCE OF 7-19; 158-179; 196-208; 450-467 AND 736-759.
 RC TISSUE=Myeloma;
 RX MEDLINE=85031810; PubMed=6092468;
 RA van Driel I.R., Stearne P.A., Grego B., Simpson R.J., Goding J.W.;
 RT "The receptor for transferrin on murine myeloma cells: one-step
 purification based on its physiology, and partial amino acid
 sequence.";
 RL J. Immunol. 133:3220-3224(1984).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=99206608; PubMed=10192390;
 RA Levy J.E., Jin O., Fujihara Y., Kuo F., Andrews N.C.;
 RT "Transferrin receptor is necessary for development of erythrocytes and
 the nervous system.";
 RL Nat. Genet. 21:396-399(1999).
 CC -1- FUNCTION: Cellular uptake of iron occurs via receptor-mediated
 endocytosis of ligand-occupied transferrin receptor into
 specialized endosomes. Endosomal acidification leads to iron
 release. The apotransferrin-receptor complex is then recycled to
 the cell surface with a return to neutral pH and the concomitant
 loss of affinity of apotransferrin for its receptor. Transferrin
 receptor is necessary for development of erythrocytes and the
 nervous system (by similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Binds one transferrin
 molecule per polypeptide chain (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (by similarity).
 CC -1- PTM: N- and O-glycosylated, phosphorylated and palmitoylated (by
 similarity). BELONGS TO PEPTIDASE FAMILY M28B.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
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 CC -----
 DR EMBL: X57349; CAA40624.1; -;
 DR EMBL: M29618; AAA37616.1; -;
 DR PIR: S29548; S29548.
 DR HSSP: P02786; ICX8.
 DR MGD: MGI:98822; TrfR.
 DR GO: GO:0006879; P:Iron ion homeostasis; IMP.
 DR InterPro: IPR003137; PA.
 DR Pfam: PF02225; PA.1.
 DR Pfam: PF04389; Peptidase_M28; 1.
 DR Pfam: PF04253; TrfR_dimer; 1.
 KM Transmembrane; Glycoprotein; Receptor; Lipoprotein; Palmitate;
 KW Signal-anchor; Endocytosis; Phosphorylation.
 FT DOMAIN 1 67
 FT TRANSMEM 68 88
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 89 763
 FT DOMAIN 572 763
 FT SITE 20 23
 FT SITE 58 61
 FT SITE 649 651
 FT LIPID 67 67
 FT MOD_RES 24 24
 FT DISULFID 89 89
 FT DISULFID 98 98
 FT CARBOHYD 104 104
 FT CARBOHYD 253 253
 FT N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT O-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT LIGAND-BINDING (BY SIMILARITY).
 FT ENDOCYTOSIS SIGNAL.
 FT STOP-TRANSFER SEQUENCE.
 FT CELL ATTACHMENT SITE (POTENTIAL).
 FT PALMITATE (BY SIMILARITY).
 FT PHOSPHORYLATION (BY SIMILARITY).
 FT INTERCHAIN (BY SIMILARITY).
 FT INTERCHAIN (BY SIMILARITY).
 FT O-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT N-LINKED (GLCNAC. . .) (BY SIMILARITY).

FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 725 725 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 730 730 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CONFLICT 25 26 LA -> AL (IN REF. 2).
 FT CONFLICT 743 743 W -> H (IN REF. 3; AA SEQUENCE).
 FT CONFLICT 757 757 W -> I (IN REF. 3; AA SEQUENCE).
 FT SEQUENCE 763 757
 SQ SEQUENCE 763 AA: 85731 MW: 832418CC26CE48B CHC64;

Query Match 18.7%; Score 435; DB 1; Length 763;
 Best Local Similarity 26.7%; Pred. No. 1.2e-24;
 Matches 123; Conservative 88; Mismatches 171; Indels 78; Gaps 14;

QY 1 MGSAAP-----DSSWGSLSKVSYNVPGFTGNFTQKKMHHSNRYINVTGRTG 56
 DB 351 MEGSCPARMNIDSCK--LELSQN-----QNKLIYKNLKKRRRLINIFGAVKG 397
 QY 57 AVEPDRIYILGHRDSWVFEGCIDPOS--GAAYHETVSPG-TLKEGMRPRRTILFASW 113
 DB 398 YEEDPRYYVVGARDA-LGAGVAARSSVGTGLLKLDAQVFSMISKDGRFRSRSTIFASW 456
 QY 114 DAEFGILGSTEMARDNSRLQERGVAVYINADSSIEGVTTLRVDCPTPLMYSLVNLTREL 173
 DB 457 TAGDFGAVGATMLEGLYSLLHKAFTYINLDKVVLGTSNFKVASPLLYTLMGKIMQDV 516
 QY 174 KSPDGEFEGRSLY--ESWTKRSPSPFSGMPRIKSLGSGNDFEVPFQRLGASGARATK 231
 DB 517 KHP---VDKSLYRDSNWISK-----VEKLSFDNAAYPPLAYSGIPAVSFCE 562
 QY 232 NMEYTKFSQYPLYSVETVELVEKFPDPMFYHLTVAOVRGMYFELANSIVLPEDCD 291
 DB 563 D-----ADYPLGTGLDYTEALQVPOQNMVRIAAEVAQOLIKLHDVBLNDYEM 616
 QY 292 YAVVLKRYADKIYINISMKHPQEMKT---YSLFDSLFAVKNFETIASFSERLQDFK 347
 DB 617 YNSKLLSF-----MKDLNQKKTDIRMGSLQWLVSARGDYPFRATRLTDFHNAEK 668
 QY 348 SNPIILRMNDQMLELRAFDPLGLPDRPFYRHVYIAPSSHN-----KYAGSPFG 399
 DB 669 TNFVAREINDRIKMYEHLSPYVSPRESFRIHWGSGSHLSALVENLKLRQKNITA 728
 QY 400 IYALDIDIESKVDPSKAMGDVKKRQISVAFTVOAAETIS 439
 DB 729 FNETLF-----RNQALATVTTIGVANALS 753

Search completed: October 4, 2003, 23:22:06
 Job time : 36 secs

[illegible]

DB	2157	TCGAAGCAGCCACAAACAGTATGCGAGGAGAAATCATTTCCCTGGATTATTTGATGACCTTTT																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							</
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TITLE	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	Toyo-oka,K., Wang,K.H., Wetzl,C., Whittaker,C., Wilming,L., Yoshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohlsuki,S. and Hayashizaki,Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 21085660 11217851 5
TITLE	JOURNAL REFERENCE AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2948)
TITLE	JOURNAL REFERENCE AUTHORS	Adachi,J., Alzawar,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukushima,S., Furuno,M., Hanagata,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiroaka,T., Hirozane,T., Hoti,F., Imotani,K., Ishii,Y., Itoh,M., Kadawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kusda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sobue,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akihira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission Submitted (16-Apr-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-resgsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT		CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/. Location/Qualifiers 1..2948 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:G630038H05" /db_xref="taxon:10090" /clone="G630038H05" /tissue_type="cortex" /clone_id="Riken full-length enriched mouse cdna library /dev_stage-"0 day neonate" 107..2175 /note="FOIATE HYDROLASE (SPTR O9DCC2, evidence: FASTY, 100&ID, 100&length, match=2256) putative" 2920..2925 /note="putative" 2948 /note="putative"
FEATURES	source	BASE COUNT 904 a 571 c 660 g 813 t ORIGIN
Query Match		60.5%; Score 1205.6; DB 11; Length 2948;
Best Local Similarity		85.3%; Pred. No. 2.8e-153;
Matches 1379; Conservative		Mismatches 234; Indels 3; Gaps 3;
Oy	241	GTTTAAATATCCCAAGCTGGCGAGGGGCCAAGAAGTAGTCCTCATCAGACCCGTGTGA 300
Dd	751	GATTAAAAATCTCAACTGCAGCGAGCGCAAAAAGCATGTATCTGTACTCAGACCCTGCTGA 810
Oy	301	CCTACTTGCTCCCTGGGGGTGAAGTCCCTATCCAGACGCGTTGGAAATCTTCCGTGGAGGTGT 360

Db	811	CTACTTTTCTCTCGGGAGAGTCCATCCAGATGGCTGGAAACCTCCCTGGAGGGTGT	870
QY	361	CCAGCGTGGAAATATCTTAAATCTGATATGTGCAGAGACCCCTCTCACACCAAGTTACCC	420
Db	871	CCAAAGTGGAAATGCTTAAATCTTAAATGAGTGCAGGTATCCCGGTCCACACCAAGTTACCC	930
QY	421	AGCAATTAATACGCTTATAGSCATATGAAATTCAGAGACCTTTGGTCTTCCAAATATTC	480
Db	931	AGCAATTAATACATGCTTATAGSCATATGAAATTCAGAAACGCTTTGGCTTCCAAATATTC	990
QY	481	TGTTTCATCCAGTTGGATATATGATGCACAGAACGCTCTAGAAAAATGGGTGCACG	540
Db	991	TGTCATCTCTTATGGATATGATATGATGCACAAACCTCTTAAACAATAGGGTGTCCAGC	1050
QY	541	ACCACCAATATGACGCTGAGAGAGAGTCCAAAGTGTCCACAAATGTGGACCTGGCTT	600
Db	1051	ACCCTTATACATGCTGAGAGAGAGTTCAAAGTGTCCACAAATGTGGACCTGGCTT	1110
QY	601	TACTGGAAATCTTCTTACACAAAAAGTCCAAAGATGCACATCCACTCTACCAATGAATGAC	660
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QY	661	GAGATTTTACATGTGATAGTACTCTCAGAGAGACAGTGGAAACCAACAGATATGTAT	720
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QY	721	TCTGGAGAGTACCCGGACATCATGGGTGTGTGTATGATATGATACCTCAGATGGAGAGC	780
Db	1231	TCTTGGAGAGTACCCGAGATGCTTGGGTATTTGGTGGCATTTGACCTCAGATGGAGAGC	1290
QY	781	TGTTGTTTATGAAACTGTGAGAGCTTTTGAACACTGAAAAAGAGGGTGGACACTAG	840
Db	1291	TGTTGTTTATGAAATTTGTGCGAGACTTTGGAACCTGAAAGAAAGAGACGAGAGCCTAG	1350
QY	841	AAGAAACAATTTTGGTTTGGCAA-GCTGGAGTGCAGAAAGATTTTGGTCTCTTGGTCTACTG	899
Db	1351	AAGAAACAATTTTGGTTTGGCAAAGCTGACAGAGCTCTTGGTCTCTTGGTCTACTG	1410
QY	899	AGTGGGCGAGAGATTAATCAAGACTCCTTCAAGAGCTGGCGCTGCTTATATTAATGCTG	959
Db	1411	AGTGGGCGAGAGAACTTCAAGAGCTCTTCAAGAGCGAGTGGCTTATATTAATGCTG	1470
QY	959	ACTCATCTATGAAAGAACTTCACTCTGAGATGTGATATGACCACTGATGTAACGCT	1019
Db	1471	ATTCCTCATGAAAGAAATTAACCTCTAAGATTTGATTCACACCACTGATGTAACGCT	1530
QY	1020	TGATATACAACTTAACAAAGAGCTGAAAGAGCCCTGATGAAGGCTTTGAAAGCAATCTC	1079
Db	1531	TAGTGTACAACTTAACAAAGAGCTGCAAAAGCCCAAGATGAAGGCTTTGAAAGAAATCTC	1590
QY	1080	TTTATGAAGTTGGACTAAAAAAGTCTTCCCAAGATTTAGTGGCATGCCCCAGAGATA	1139
Db	1591	TTTATGAAGTGTGGAAGAAAGAGTCTTCACTGATTTATTTAGGAATGGCCAGAAATA	1650
QY	1140	GCAAAATTTGGATCTGGAATATGATTTTGGAGTCTTCCCAAGCACTTGGAAATGGCTCAG	1199
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QY	1200	GCAGAGCAGGTATCTAAAAAATTGGGAACAAACAAATTACAGGCTATCCACTGATC	1259
Db	1711	GCAGAGCCCCGATTAATCTAAAAAATTGGGAACAAACAAAGCTACAGCTATCCCTCATC	1770
QY	1260	ACAGTCTATGAACAAATATGATGTTGGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1319
Db	1771	ACAGTCTATGAACAAATATGATGCTGGATGAATATTTTATGACCAACATTTTAAATATC	1830
QY	1320	ACCTCACTGTGGCCAGGTTGAGAGAGGATGATGTTGAGCTAGCCATTCATATAGTC	1379
Db	1831	ACCTCACTGTGGCCAGGTTGAGAGAGGATGATGTTTGAACCTTGCCAAATTCATATAGTC	1890
QY	1380	TTCCTTTTGAATTTGTCAGATTAATGCTGTAGTTTTTAAAGAACTATGCTGACAAATCTTACA	1439

Db 1891 TTCCTTTGACCTGCCAAAGTTATGCTGTACCTGTGAAGAAGTATGCTAGACATATCTACA 1950
 QY 1440 ATATTTCTATGAACATCCACAGAAATGAAGACATACAGTTATCATTTGATTCACCTT 1499
 Db 1951 ATATTTCAATGAACATCCACAGAAATGAAGCTTTCATGATATCTTTGATTCACCTT 2010
 QY 1500 TTTCTGAGTAAATAATTTTACAGAAATGCTTCCAGATTCCAGGAGACCTCCAGGA-C 1558
 Db 2011 TTTCTGAGTAAATAATTTTACAGATGTTCATCTAGTCAATTCACAGAGCTCCAGAGG 2070
 QY 1559 TTTGACAAAAGCAACCAATATGTTTGAAGATGATGATATCATCATGATTTCTGGAA 1618
 Db 2071 TTTGACAAAAGCAACCAATATGTTTGAAGATGATGATATCATCATGATTTCTGGAA 2130
 QY 1619 AGAGCATTTTATGATTCATGAGGTTTACAGACAGACCTTTTATAGCATATCATAT 1678
 Db 2131 CGTGCATTCATTCATTCCTTTAGGCTTTCACAGAAAGGCTTCTTGAAGCATATCATAT 2190
 QY 1679 GCTCCAGACGACCAACAAGTATGACAGGGAGTCAATCCAGGAATTTATGATCTGTG 1738
 Db 2191 GCTCCAGACGACCAACAAGTATGACAGGAATCATTTCCCTGGATTTATGATGCTCT 2250
 QY 1739 TTTGATTTTGAAGCAAGTGAACCTTCCAGAGGCTTCCAGAGATGTTGAAGACATAT 1798
 Db 2251 TTTGATTTTGAAGCAAGTGAACCTTCCAGAGGCTTCCAGAGATGTTGAAGACATAT 2310
 QY 1799 TCT-GTTCAGACCTTTCACAGTGCAGGAGCTGCAGAGACTTTGAGTGAAGTACCT 1853
 Db 2311 TCTAGTTGCAACCTTTTACAGTGCAGAGCTGCAGAGACTTGTAGGGGACAGCTCT 2366

RESULT 3
 AL532732 1201 bp mRNA linear EST 23-MAY-2003
 LOCUS AL532732 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DN001YK13 5-PRIME, mRNA sequence.

ACCESSION AL532732
 VERSION AL532732.2 GI:31070564
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1201)

REFERENCE
 AUTHORS Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12796225.

CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5903.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DN001YK13&cluster=5903.r. Contact :
 Peng Liang Email: filiang@life.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DN001YK13

FEATURES

source

1. 1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DN001YK13"
 /tissue_type="ADULT BRAIN"
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 /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6

BASE COUNT 340 a 231 c 312 g 294 t 24 others
 ORIGIN
 Query Match 46.9%; Score 933.4; DB 9; Length 1201;
 Best Local Similarly 97.6%; Pred. No. 1.7e-116;
 Matches 973; Conservative 5; Mismatches 16; Indels 3; Gaps 3;

vector. Library was not normalized."

240 AGGTTAAATATGCCACGTGCGAGGGGCGCAAGAGAGATCTTCTACTACAGACCTTCG 299
 Db 75 AGGTTAAATATGCCACGTGCGAGGGGCGCAAGAGAGATCTTCTACTACAGACCTTCG 134
 QY 300 ACTACTTGTCTCTGGGGAAGTCCATTCACAGCGTGTGAATCTTCCGAGAGTGTG 359
 Db 135 ACTACTTGTCTCTGGGGAAGTCCATTCACAGCGTGTGAATCTTCCGAGAGTGTG 194
 QY 360 TCCAGCGTGAATATATCTTAATCTGAATGTGACAGACACCTCTCACACGATTACC 419
 Db 195 TCCAGCGTGAATATATCTTAATCTGAATGTGACAGACACCTCTCACACGATTACC 254
 QY 420 CAGCAATGATATACGCTTATAGGCAATGAGATTCAGAGAGCTGTGGTCTCCAGTATTC 479
 Db 255 CAGCAATGATATATGCTTATAGGCAATGAGATTCAGAGAGCTGTGGTCTCCAGTATTC 314
 QY 480 CTGTTCATCCAGTTGATATGATGACAGAGAGCTCTAGAAAAAATGGTGGCTCAG 539
 Db 315 CTGTTCATCCAGTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 374
 QY 540 CACCACCATATGACAGCTGAGAGAGAGTCAAAAGTCTCAATGTTGACCTGGCT 599
 Db 375 CACCACCATATGACAGCTGAGAGAGAGTCTCAAAAGTCTCAATGTTGACCTGGCT 434
 QY 600 TTTACTGGAACCTTTTACACAAAAGTCAAGATGCAATCCACTACCAATGAAGTGA 659
 Db 435 TTTACTGGAACCTTTTACACAAAAGTCAAGATGCAATCCACTACCAATGAAGTGA 494
 QY 660 CGAATATTTCAATATGATAGTACTCTCAGAGAGAGCTGGAACAGACAGATATGTCA 719
 Db 495 CGAATATTTCAATATGATAGTACTCTCAGAGAGAGCTGGAACAGACAGATATGTCA 554
 QY 720 TTTGGAGGTCACCGGAGCTCATGGGTGTTGGTATTTGAACCTCAGAGTGAAGCAG 779
 Db 555 TTTGGAGGTCACCGGAGCTCATGGGTGTTGGTATTTGAACCTCAGAGTGAAGCAG 614
 QY 780 CTGTGTTCATGAAACGTGAGAGAGCTTGAACACAGTGAAGAGAGTGAAGCTTA 839
 Db 615 CTGTGTTCATGAAACGTGAGAGAGCTTGAACACAGTGAAGAGAGTGAAGCTTA 674
 QY 840 GAAGAACAATTTGTTTGAAGCTGGAGTGCAGAGAAATTTGGTCTTCTGTTCTACTG 899
 Db 675 GAAGAACAATTTGTTTGAAGCTGGAGTGCAGAGAAATTTGGTCTTCTGTTCTACTG 734
 QY 900 AGTGGCAGAGGATTAATCAAGACTCTTAAGAGCTGGCGTGTATTAATAGCTG 959
 Db 735 AGTGGCAGAGGATTAATCAAGACTCTTAAGAGCTGGCGTGTATTAATAGCTG 794
 QY 960 ACTCATCTATAGAAGAACTACACCTGAGATGATTTGATTAACACAGTATGATAGCT 1019
 Db 795 ACTCATCTATAGAAGAACTACACCTGAGATGATTTGATTAACACAGTATGATAGCT 854
 QY 1020 TGGTATACCACTTACAAAAGAGCTGAAAAGCCTGATGAAGCTTTGAAGCAAAATCTC 1079
 Db 855 TGGTATACCACTTACAAAAGAGCTGAAAAGCCTGATGAAGCTTTGAAGCAAAATCTC 914
 QY 1080 TTTATGAAGTTGAGACTAAAAAAGTCTTCCCAAGATTCAGTGCATGCCAGATTA 1139
 Db 915 TTTATGAAGTTGAGACTAAAAAAGTCTTCCCAAGATTCAGTGCATGCCAGATTA 974
 QY 1140 GCAATTTGGATGTGGAATGATTTTGGAGTCTTCCCAAGATTCAGTGCATGCCAGATTA 1199
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 QY 1200 GCAGAGCAGCGTATTAATAAATTTGGGAAACAACAA 1236

DB 1033 GC-GRACACGGTATCTAAATAATGGGAACAACAA 1068

RESULT 4
AL563970/c 1201 bp mRNA 1linear EST 31-MAY-2003
LOCUS AL563970 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM001YE22 3-PRIME, mRNA sequence.
ACCESSION AL563970
VERSION AL563970.2 GI:31287955
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 15, 2001 this sequence version replaced gi:12913887.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 101 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5903.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DM001BCLINP1&cluster=5903.r. Contact :
Peng Liang Email: fliang@lifetech.com URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Fairway Avenue Genoscope sequence ID : CS0DM001BCLINP1.
Location/Qualifiers
1. 1201
/organism="Homo sapiens"
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/clone="CS0DM001YE22"
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/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: Liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 342 a 251 c 212 g 333 t 63 others
ORIGIN

Query Match 45.2%; Score 900.4; DB 9; Length 1201;
Best Local Similarity 92.2%; Pred. No. 4.7e-112;
Matches 1022; Conservative 29; Mismatches 47; Indels 11; Gaps 10;

QY 844 AACAAATTTGTTGCAACCTGGAGTCAGAGAAATTTGCTCTCTGCTCTACTGAGTG 903
DB 1101 AACACAAATTTTTCATACCTGRTTCAMAAAATTTGCTTC-TKGTTCACGAGTG 1043
QY 904 GGCACAGATTAATTAAGACTCTTCAAGAGCGTGGCTTATTAATGCTGACTG 963
DB 1042 GWCAGAGGAGATTGADG-CYCTCTCAGAGAGCGTGGCT-GCTTATTAATGCTG-MBC 986
QY 964 ATCTATAGAGGAACCTACTCTGAGAGTTGATTGTA-CACCACTGATGACAGTTGG 1022
DB 985 ATCTATAG-ARGAACTACACTCTGAGATTGATTGTAACCGCTGATGTAACMC-TKG 928
QY 1023 TATTAACCTTAACAAAGAGCTGAAGAGCCCTGATGAGGCTTTGAAGCAATCTCTT 1082
DB 927 TACACAACTTAACAAAGGCTG-AAAGCCCTGATGAGGCTTTGAAGCAATCTCTT 869
QY 1083 ATGAAGTTGCACTAAAAAAGCTCTCCCAAGAGTTGAGTGCATGCCAGAGATAAGCA 1142
DB 868 ATGAAG-TGCACTAAAAAAGCTCTCTCCCAAGAGTTGAGTGCATGCCAGAGATAAGCA 810

QY 1143 AATGGGATCTGGAAATGATTTTGGAGTGTCTCCACAGACTGGAAATGCTTACGCA 1202
DB 809 AATGGGATCTGGAAATGATTTTGGAGTGTCTCCACAGACTGGAAATGCTTACGCA 750
QY 1203 GAGCAGCTATACATAAATTTGGGAACAACAATTCAGCGGCTATCCAGTATCACA 1262
DB 749 GAGCAGCTATACATAAATTTGGGAACAACAATTCAGCGGCTATCCAGTATCACA 690
QY 1263 GTCCTATGAACATATGATGTTGGGAAGTTTATATCATATGTTTAAATATCAC 1322
DB 689 GTGCTATGAACATATGATGTTGGGAAGTTTATATCATATGTTTAAATATCAC 630
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DB 329 CATTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 270
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DB 209 ATATTGAAGCAAGTGGACCTTCCAAAGCGTGGGAGATGTAAGAGACAGATTTCTG 150
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QY 1863 CTTTGAAGCAAGTGGACCTTCCAAAGCGTGGGAGATGTAAGAGACAGATTTCTG 1920
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DB 29 TATTGATTAATTTTAAATTTGATATTT 1

RESULT 5
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LOCUS AL532691 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
DEFINITION CS0DN001YK13 3-PRIME, mRNA sequence.
ACCESSION AL532691
VERSION AL532691.2 GI:31070523
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization

1036	AAAAAGACCTGAAAAAGCCCTGATGGAAGGCTTTGAAGGCAAAATCTGTTATGAAGCTGGAC	1095
Db	61 AAAAGAGCTGAAAAAGCCCTGATGGAAGGCTTTGAAGGCAAAATCTGTTATGAAGTGGAC	120
QY	1096 TAAAAAAAAGTCCTTCCCGAGATTCAGTGGCATGCCCGATGAACAATTTGGGATCTGG	1155
Db	121 TAAAAAAAAGTCCTTCCCGAGATTCAGTGGCATGCCCGATGAACAATTTGGGATCTGG	180
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QY	1336 GGTTCGAGGAGGAGTGTGTGTTGAGCTAGCCAAATTCATAGTGTCTCCCTTTGATGTGCG	1395
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Db	661 ATTATGAGTTACAGACAGACCTTTTATGAGCATGTCTATGCTCCACAGACACAA	720
QY	1696 CAAATGATCCAGGAGGATCATTCGCCAGAAATTTATGATGCTGTGT -GATATGAAACA	1754
Db	721 CCAGTATCCAGGAGGATCATTCGCCAGAAATTTATGATGCTGTGTGATATGAAAC	780
QY	1755 AAGTGGACCTTTCCAGAGCCCTGGG ---GAGTGTCAACAGACAGATTTCTGTGACGCT	1811
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LOCUS	Bg208080	776 bp mRNA linear EST 21-APR-2001
DEFINITION	R5727570	Atherisys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION	Bg208080	
VERSION	Bg208080.1	GI:13729767
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 776)	
AUTHORS	Harrington,J.,J.,Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,K., Ramchandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith ,E., Veloso,N., Kliska,A., Hess,J., Colthen,K., Lo,K., Offenbacher	

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	/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
High quality sequence stop: 453.	
Location/Qualifiers	
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BASE COUNT	230 a 157 c 127 g 262 t
ORIGIN	
Query Match	37.7%; Score 751.4; DB 10; Length 776;
Best Local Similarity	99.1%; Pred. No. 6.2e-92;
Matches 766; Conservative	0; Mismatches 6; Indels 1; Gaps 1;
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Y	1278 ATGAGTTGGTGGAAAAAGTTTATGATCCAAATGTTAAATATACCTCAGTCAGGCCAGG 13378
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Y	1338 TTCGAGGAGGAGTGTGTTTGAAGTACGCCAATCCAAATGTCCTCCCTTTGATTGTCGAG 13979
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Y	1398 ATTATGCGTGTGTTTAAAGATGTGTGTGCAAAAATCAATAATTTCTATGAACATC 1457
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Y	1458 CACAGGAATGAGACATACAGTGTATATTTGATTCACTTTTCTGACAGTAAAAAATT 15119
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Y	1518 TTACAGAAATTGCTTCCAAAGTTCAGCGAGAGACTCCAGAGCTTGCACAAAAGCAACCAA 15777
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Y	1638 TAGGTTTACACAGAGACTTTTATATAGCATGTATATGTCACAGCAGCACAACA 16977
Db	353 TAGGTTTACACAGAGACTTTTATATAGCATGTATATGTCACAGCAGCACAACA 294
Y	1698 AGTATGACAGGAGATCATTCACAGAAATTATGATGCTCTGTTTGATATGGAAGCAAG 1757
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Y	1758 TGGACCCCTTCCAAAGCCCTGGGGAGATGGAAGAGACAAATTCGTGACACCCCTTCCAG 1817
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QY	1818	TGCAGGAGCCTGCAGAGACTTTGAGTGAAGTAGCCTAAGAGACTTCTTAGAGACTCGT	1877
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QY	1878	ATTGAATTTGGTGTATGTCACCCAAAGAAATTAATGGGTATATTGATTAATTTTAAA	1937
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QY	1938	ATTGCTATATTGTGAATTAAGATTGAATTTATATATAAAAAAAAAAAAAAAAAAAAA	1990
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RESULT	9
LOCUS	BGI194269
DEFINITION	BGI194269 767 bp mRNA linear EST 21-APR-2001
ACCESSION	R811413 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
VERSION	BGI194269
KEYWORDS	BGI194269.1 GI:13715956
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE
AUTHORS
1 (bases 1 to 767)
Harrington, J. T., Sherf, B., Rundlett, S., Jackson, P. D.
Primates; Catarrhini; Homidae; Homo.

TITLE	Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL	Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE	21227151

COMMENT
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9586
Email: scotcain@atersys.com
High quality sequence stop: 550.
11

FEATURES	
source	Location/Qualifiers
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/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
235 a 142 c 198 g 190 t 2 Others

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Query Match	37.4%;	Score 745.4;	DB 10;	Length 767;
Best Local Similarity	98.3%;	Pred. No. 4e-91;		
Matches 752; Conservative	0;	Mismatches 13;	Indels 0;	

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QY	1242	GGGGGTATCCACTGTATCATCAGAGTGTCTATGAACATATGAGTTGG	1286
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RESULT 10

AI050871/

LOCUS
DEFINITIO

ACCESSION
VERSION

KEYWORDS

SOURCE ORGANISM

REFERENCE

TITLE

JOURNAL
COMMENT

A1050871
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).contains Alu repetitive element; mRNA sequence.
 A1050871
 A1050871.1 GI:3307676
 EST.
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 Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 770)
 NC1/NIHDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BTCAP), Tumor Gene Index
 unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 clone distribution: NC1-CGAP clone distribution Information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www.bio.lnl.gov/bdrrp/image/image.html
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Db 787 GCAGCCACAA 796

RESULT 12
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LOCUS
DEFINITION
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similar to SW:PSM.HUMAN 004609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN
; mRNA sequence.
BF940223
BF940223.1 GI:12357531
EST.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 720)
NCI/NIHNS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLN, send email to:
info@image.llnl.gov
Seq primer: -400P from Gibco
High quality sequence stop: 463.
Location/Qualifiers

FEATURES

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modified polylinker; Site-1: Not I; Site-2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAACTGAGCGGCGGATATCTTTTATTTTATTTTATTTT
T 3']]; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 221 a 157 c 116 g 225 t 1 others

ORIGIN

Query Match 33.9%; Score 674.6; DB 10; Length 720;
Best Local Similarity 96.9%; Pred. No. 1.4e-81;
Matches 698; Conservative 0; Mismatches 20; Indels 2; Gaps 1;

QY 1236 TATCAGAGTCTATGAAACATATAGTGTGGGAAAGTTTATATCCATGTTTAA 1315
Db 720 TATCCAGTGTCTATGAAACATATAGTGTGGGAAAGTTTATATCCATGTTTAA 661
QY 1316 TATCAGTCTGCTGCGCCAGGTTGAGAGAGGATGTTGAGCTAGCCAAATTCATA 1375
Db 660 TATCAGTCTGCTGCGCCAGGTTGAGAGAGGATGTTGAGCTAGCCAAATTCATA 601
QY 1376 GTGCTCCCTTTGATGTGCGAGATTAATCTGTAGTTTAAAGAAATGATGTCATA 1435
Db 600 GTGCTCCCTTTGATGTGCGAGATTAATCTGTAGTTTAAAGAAATGATGTCATA 541
QY 1436 TACATATTTCTATGAAACATCCACAGGAAATGAGACATACATGATGATGATGATGATGATGAT 1495
Db 540 TACAGTATTTCTATGAAACATCCACAGGAAATGAGACATACATGATGATGATGATGATGATGAT 481
QY 1496 CTTTCTTCTGAGTAAAAATTTTACAGAAATTCCTTCCAGATTCACGAGAGAGCTCAG 1555
Db 480 CTTTCTTCTGAGTAAAAATTTTACAGAAATTCCTTCCAGATTCACGAGAGAGCTCAG 421
QY 1556 GACTTGTACAAAACCAACCAATGTTGTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1615
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QY 1616 GAAAGACATTTATGATCCATTAGGTTTACAGAGAGAGCTTTTATAGCANTGATC 1675
Db 360 GAAAGACATTTATGATCCATTAGGTTTACAGAGAGAGCTTTTATAGCANTGATC 301
QY 1676 TATGCTCCAGAGCCACCAACAAGTATGACAGGAGATCATTCACAGAAATTTATGATGCT 1735
Db 300 TATGCTCCAGAGCCACCAACAAGTATGACAGGAGATCATTCACAGAAATTTATGATGCT 241
QY 1736 CTGTGTGATATTAAGCAAGAGGACCCCTCCAAAGCCTGGGAGATGTGAAGACAG 1795
Db 240 CTGTGTGATATTAAGCAAGAGGACCCCTCCAAAGCCTGGGAGATGTGAAGACAG 181
QY 1796 ATTTCTGTTGACGCTTCCAGAGTCCAGAGCTGACAGACTTTGATGAATAGCTTA 1855
Db 180 ATTTATGTTGACGCTTCCAGAGTCCAGAGCTGACAGACTTTGATGAATAGCTTA 121
QY 1856 GAGGATCTTTGAGACTGTATGAAATTTGTGTGATGTCATCTC--AAAGATTAATA 1913
Db 120 GAGGATCTTTGAGAAATCCGATTAATTTGTGTGATGTCATCTCAGAAAGATTCGA 61
QY 1914 ATGGTATATGATTAATTTTAAATTTGATATTTGAAATTAAGTGAATTAATATAT 1973
Db 60 ATGGTATATGATTAATTTTAAATTTGATATTTGAAATTAAGTGAATTAATATAT 1

RESULT 13
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LOCUS tve4912.x1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:2283910 3'
DEFINITION similar to gb:M99467 PROSTATE-SPECIFIC MEMBRANE ANTIGEN (HUMAN);,
mRNA sequence.
ACCESSION Al672408
VERSION Al672408
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Enxayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 (bases 1 to 690)
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdpr/image/image.html
Insert Length: 945 Std Error: 0.00
Seq primer: -400P from Glbco
High quality sequence stop: 454.
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/clone_lib="NCI CGAP Kid1"
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site:1: Not I; Site:2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."
BASE COUNT 211 a 152 c 110 g 212 t 5 others
ORIGIN
Query Match 31.4%; Score 625.4; DB 9; Length 690;
Best Local Similarity 95.7%; Pred. No. 5.9e-75;
Matches 662; Conservative 0; Mismatches 26; Indels 4; Gaps 2;
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DB 690 TGGTGAAGAAAGTTTATGATC- AATGTTTAAATATCAACCTGAGCCAGGTCGAG 633
OY 1344 GAGGGATGCTGTTGAGCTACCAATTCATAGTCTCCCTTTGATTTGAGATTAATG 1403
DB 632 GAGGGATGCTGTTGAGCTACCAATTCATAGTCTCCCTTTGATTTGAGATTAATG 573
OY 1404 CTGTAGTTTAAAGAAAGTATGCTGACAAATCTCAATATTTCTATGAAACATCCACAG 1463
DB 572 CTGTAGTTTAAAGAAAGTATGCTGACAAATCTCAATATTTCTATGAAACATCCACAG 513
OY 1464 AAATGAGACATACATGTTTATCATTTGATTCACCTTTTTCGAGTAAAAAATTTTACAG 1523
DB 512 AAATGAGACATACATGTTTATCATTTGATTCACCTTTTTCGAGTAAAAAATTTTACAG 453
OY 1524 AAATGCTTCCAAAGTTCAGCAGAGACTCCAGACTTTGACAAAGCAACCAATATTGT 1583

RESULT 14
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LOCUS AGENCOURT.10809202 MAPCL Homo sapiens cDNA clone IMAGE:6720185 5',
DEFINITION mRNA sequence.
ACCESSION CA488428
VERSION CA488428.1 GI:24950277
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Enxayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 (bases 1 to 916)
TITLE NIH-MGC <http://mgc.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLAM14279 row: e column: 17
High quality sequence stop: 448.
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/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hERT-HMEL
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/clone_lib="MAPCL"
/note="Vector: pCMV-SPORT6; Site:1: EcoRV; Site:2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.


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OY 1688 AGCCACACAGATATGACGGGAGTCATCCACAGAAATTATGATGCTGTGTTGATAT 1747
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Db 306 AGCCACACAGATATGACGGGAGTCATCCACAGAAATTATGATGCTGTGTTGATAT 247
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OY 1748 GAAAGCAAAAGTGAACCTTCCAGAGGCTGGGGAGATGTGAAGAGACAGATTTCGTGCA 1807
    |||||||
Db 246 GAAAGCAAAAGTGAACCTTCCAGAGGCTGGGGAGAGTGAAGAGACAGATTTCGTGCA 187
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OY 1808 GCCTTCACAGTGCAGGAGCTGCAGACCTTGTAGTGAAGTGAAGGCTTAAGAGATTCCTTA 1867
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Db 186 GCCTTCACAGTGCAGGAGCTGCAGACCTTGTAGTGAAGTGAAGGATTCCTTA 127
    |||||||
OY 1868 GAGACTCTGATTTGATTTGTGTATGTCACCTC--AAAGATATATATGCTATATG 1925
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Db 126 GAGATTCGATTTGATTTGTGTATGTCACCTCAGAGAAATCGTATATGCTATATG 67
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OY 1926 ATAAATTTTAAATTTGTATATTTGAATAAAAGTTGAATTTATATATATAAAAAA 1985
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Db 66 ATAAATTTTAAATTTGTATATTTGAATAAAAGTTGAATTTATATATATAAAAAA 7
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OY 1986 AAAAAA 1991
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Db 6 AAAAAA 1

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Search completed: October 4, 2003, 20:55:20
 job time : 5070 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2003, 10:14:18 ; Search time 9490 Seconds

(without alignments)
8587.142 Million cell updates/sec

Title: US-09-973-382C-1

Perfect score: 1992

Sequence: 1 agcaatactactaccacac.....taaaaaaaaaaaaaaaaa 1992

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapept 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_ov:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rtd:*

36: em_hcg_mam:*

37: em_hcg_vrt:*

38: em_sy:*

39: em_hgtgo_hum:*

40: em_hgtgo_mus:*

41: em_hgtgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1992	100.0	1992	9	AF261715 Homo sapi
2	1702.6	85.5	2653	6	AX337498 Sequence
3	1702.6	85.5	2653	6	AX505108 Sequence
4	1702.6	85.5	2653	6	123794 Sequence 1
5	1702.6	85.5	2653	6	HUMPSM
6	1690.6	84.7	2518	9	AF176574 Homo sapi
7	1687.2	79.5	2253	6	AX376036 Sequence
8	1584	79.5	2253	6	AX467227 Sequence
9	1582.4	75.9	2253	9	AY101595 Homo sapi
10	1511.4	70.9	2472	9	BC025672 Homo sapi
11	1412.4	68.9	2061	6	AX403107 Sequence
12	1371.6	68.9	2532	4	AF050502 Sus scrofa
13	1263.6	63.4	2899	10	RNU75973
14	1257.2	63.1	2348	10	AF040256
15	1254.4	63.0	2259	10	AF513486 Rattus no
16	1251.8	62.8	2603	10	AF026380 Mus muscu
17	1084.8	54.5	1428	10	AF039707 Rattus no
18	885.4	44.4	3171	6	AX136153 Sequence
19	885.4	44.4	3171	6	BD123529
20	885.4	44.4	3171	9	AK075390 Homo sapi
21	883.8	44.4	3152	6	AX006438 Sequence
22	883.8	44.4	3152	9	HSN012370 Homo sapi
23	860.6	43.2	2690	10	AY243507
24	684.6	34.4	2431	5	BC049312 Dantio rer
25	561.2	28.2	710	9	AF027824 Homo sapi
26	428	21.5	13788	2	AP003122 Homo sapi
27	428	21.5	192648	2	AC024234 Homo sapi
28	423.2	21.2	40131	2	AC136711 Homo sapi
29	412	20.7	93525	9	AF007544 Homo sapi
30	410.4	20.6	156255	2	AP002369 Homo sapi
31	410.4	20.6	157527	2	AC117746 Homo sapi
32	410.4	20.6	158524	2	AL162372 Homo sapi
33	410.4	20.6	187529	9	AC118273 Homo sapi
34	410.4	20.6	246865	2	AC074003 Homo sapi
35	403.2	20.2	573	9	AF254357 Homo sapi
36	330	16.6	455	9	AF254358 Homo sapi
37	312.4	15.7	192648	2	AC024234 Homo sapi
38	290.8	14.6	156255	2	AP002369 Homo sapi
39	229.4	11.5	170102	9	AC009237 Homo sapi
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ALIGNMENTS

RESULT 1

LOCUS AF261715

DEFINITION Homo sapiens prostate-specific membrane antigen-like protein (PSMA/GCP III) mRNA, complete cds.

ACCESSION AF261715

VERSION AF261715.1 GI:11078563

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1992)

O'Keefe,D.S., Bacich,D.J. and Heston,W.D.W.

Cloning and Characterization of a novel glutamate-preferring

peptidase that maps to the SCZDII locus: a candidate gene for Schizophrenia?

JOURNAL
REFERENCE
AUTHORS
TITLE
2 (bases 1 to 1992)
O'Keefe,D.S., Baclich,D.J. and Heston,W.D.W.
Expression Profile of Prostate-Specific Membrane Antigen (PSMA) Versus a Prostate-Specific Antigen-Like Gene in Normal Tissues, Prostate Cancer and Tumor Associated-Vasculature

JOURNAL
REFERENCE
AUTHORS
TITLE
Unpublished
3 (bases 1 to 1992)
O'Keefe,D.S., Baclich,D.J. and Heston,W.D.W.
Direct Submission
Submitted (27-APR-2000) Cancer Biology, Cleveland Clinic Foundation, NB 40, 9500 Euclid Avenue, Cleveland, OH 44195, USA

FEATURES
source
Location/Qualifiers
1. 1992

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/note="maps to Schizophrenia Disorder Type II locus"
1. 1992
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527..1855
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/note="glutamate carboxypeptidase II; similar to Homo sapiens PSMA; folate hydrolyase-like; member of the M28 peptidase family; formed by duplication of the PSMA gene"
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BASE COUNT 638 a 352 c 451 g 551 t

Query Match 100.0%; Score 1992; DB 9; Length 1992;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1992; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1741	TGATATTTGAAAGCAAGTGAAGCCCTTCAGAGCCCTGGGGAGATGTGAAGACAGATTTC	1800
QY	1801	TGTTGCAACCTTCACAGTGCAGGACGCTGCAGACATTTTGATGTAAGTACGCTTAAGAGA	1860
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QY	1861	TTCTTTTGAGAGCTCTGATTTGAATTTTGTCGTATGTCACCAAGAAATATATATGGGTA	1920
Db	1861	TTCTTTTGAGAGCTCTGATTTGAATTTTGTCGTATGTCACCAAGAAATATATATGGGTA	1920
QY	1921	TATTTGATTAATTTTAAAAATTTGGTATTTTGAATTAAGTTGAATTTATATATAAAAAA	1980
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QY	1981	AAAAAAAAAAAAA 1992	
Db	1981	AAAAAAAAAAAAA 1992	
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LOCUS	AX337498	2653 bp	DNA linear PAT 09-JAN-2002
DEFINITION	Sequence 8007 from Patent WO0194629.		
ACCESSION	AX337498		
VERSION	AX337498.1	GI:18128217	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,		
AUTHORS	Horrijgan,S., Soppel,D.R. and Weaver,Z.		
TITLE	Cancer gene determination and therapeutic screening using signature		
JOURNAL	gene sets		
FEATURES	Patent: WO 0194629-A 8007 13-DEC-2001;		
source	Avalon Pharmaceuticals (US)		
BASE COUNT	Location/Qualifiers		
ORIGIN	1..2653		
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	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
Query Match	85.5%;	Score 1702.6;	DB 6; Length 2653;
Best Local Similarity	98.5%;	Pred. No. 0;	
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QY	240	AGGTTAAAAATGCCACCTGGCAGGGCCAAAGAGTCATTTCTACTCAGACCCGCTG	299

Db	899	AGGTTAAAAATGCCAGCTGGCAGGAGGCCAAAGAGTCATTTCTACTCCAGCCCTGCTG	958
QY	300	ACTACTTTTGCTCCTGGGGTGAAGTCCCTATCCAGAGCGTGTGAATCTTCCGTGAGGGTGG	359
Db	959	ACTACTTTGCTCCTGGGGTGAAGTCCCTATCCAGATGGTTGGAATTTCTCTGSAAGGTTGGT	1018
QY	360	TCGACCGGTGGAATATCTCTAAATCTGAATGGTGCAGAGAGACCTCTCAACACAGGTTAC	419
Db	1019	TCACAGCTGGAAATATCTCTAAATCTGAATGGTGCAGAGAGACCTCTCAACACAGGTTAC	1078
QY	420	CAGCAAAATGAATACCCCTTATAGAGCTGGAATTTGCGAGAGCGTGTGCTTCCAGATATTC	479
Db	1079	CAGCAAAATGAATATCTCTTATAGCGCTGGAATTTGCGAGAGCGTGTGCTTCCAGATATTC	1138
QY	480	CTGTTTCATCCAGTGTGATACCTATGATGACAGAACTCCTCTGAAAAATGGGTGGCTCAG	539
Db	1139	CTGTTTCATCCAGTGTGATACCTATGATGACAGAACTCCTCTGAAAAATGGGTGGCTCAG	1198
QY	540	CACCACCAAGATAGCAGCTGGAGAGAGAGTCTCAAGTGTCTCTACAAATGTGGACCTGGCT	599
Db	1199	CACCACCAAGATAGCAGCTGGAGAGAGAGTCTCAAGTGTCTCTACAAATGTGGACCTGGCT	1258
QY	600	TTACTGGAACCTTTTCTACACAAAAAGTCAGATCCACATCCACTCTACCAATGAATGA	659
Db	1259	TTACTGGAACCTTTTCTACACAAAAAGTCAGATCCACATCCACTCTACCAATGAATGA	1318
QY	660	CGAGAAATTTACAATGTGATAGTACTCTCAGAGGAGCGATGGGAACAGACAGATATGTCA	719
Db	1319	CAGAAATTTACAATGTGATAGTACTCTCAGAGGAGCGATGGGAACAGACAGATATGTCA	1378
QY	720	TTTCGGGAGGTCACCGGGAGCTCATGGGTGTGTGGTATTTGATTCACCTCAGAGTGGAGCAG	779
Db	1379	TTTCGGGAGGTCACCGGGAGCTCATGGGTGTGTGGTATTTGATTCACCTCAGAGTGGAGCAG	1438
QY	780	CTGTTGTTTCATGAAGAACTGTGAGAGACTTTGGAACCTGAAAAAGGAAGGGTGGAGACTA	839
Db	1439	CTGTTGTTTCATGAAGAAATTTGTGAGAGACTTTGGAACCTGAAAAAGGAAGGGTGGAGACTA	1498
QY	840	GAAGAACAAATTTTGTTCGAAGCTGGATGACAGAAATTTGGTCTTCTTGAGTCTACTG	899
Db	1499	GAAGAACAAATTTTGTTCGAAGCTGGATGACAGAAATTTGGTCTTCTTGAGTCTACTG	1558
QY	900	AGTGGGCGAGAGATATTTCAAGACTCCTTCAAGACCGTGGCGTGTATATTAATGCTG	959
Db	1559	AGTGGGCGAGAGAGATATTTCAAGACTCCTTCAAGACCGTGGCGTGTATATTAATGCTG	1618
QY	960	ACTACTCTATGAGAGGAACCTACACTCTGAGAGTGGATTTGACACCACTGATGACAGCT	1019
Db	1619	ACTACTCTATGAGAGGAACCTACACTCTGAGAGTGGATTTGACACCACTGATGACAGCT	1678
QY	1020	TGATATACACCTTACAAAGAGCGTGAAGACCCGATGAAGGCTTGAAGGCAAAATCTC	1079
Db	1679	TGATATACACCTTACAAAGAGCGTGAAGACCCGATGAAGGCTTGAAGGCAAAATCTC	1738
QY	1080	TTTATGAAGTTTGACATAAAAAAGTCCCTCCCAAGATCTCAGTGGCATGCGCCAGGATTA	1139
Db	1739	TTTATGAAGTTTGACATAAAAAAGTCCCTCCCAAGATCTCAGTGGCATGCGCCAGGATTA	1798
QY	1140	GCAAAATTTGGATCTGGGAATGATATTTGAGGTGTTCTTCAACGACTTGGAAATTCCTCAG	1199
Db	1799	GCAAAATTTGGATCTGGGAATGATATTTGAGGTGTTCTTCAACGACTTGGAAATTCCTCAG	1858
QY	1200	GCAGAGCAGCGTATCTATAAAAAATTGGGGAACAAACAAATTCAGGGCGTATCCACTGTATC	1259
Db	1859	GCAGAGCAGCGTATCTATAAAAAATTGGGGAACAAACAAATTCAGGGCGTATCCACTGTATC	1918
QY	1260	ACAGTGTCTATGAAGAACATATGAGTTGGTGAAGTTTATGATCCAAATGTTTAAATATC	1319
Db	1919	ACAGTGTCTATGAAGAACATATGAGTTGGTGAAGTTTATGATCCAAATGTTTAAATATC	1978
QY	1320	ACCTCACTGTGGCCAGCTTGGAGAGGAGATGCTGTTGAGCTAGACCAATTCATPATGCTC	1379
Db	1979	ACCTCACTGTGGCCAGCTTGGAGAGGAGATGCTGTTGAGCTAGACCAATTCATPATGCTC	2038

OY		1202	TGGATTTCAACCTTAACAAAAGAGGTGAAAGGCCCTGATTGAAGGCTTGAAGGCACAATCTC	1079
Db		1679	TGGTACCAACCTTACAAAAAGAGTCGAAAGCCCTGATGAAAGGCTTTGAAGGCAAATCTC	1738
OY		1080	TTTTATGAAAGTTGGACTTAAAAAAAGTCCCTCCAGAGTTCAGTGCGATCCCCAGATAA	1139
Db		1739	TTTTATGAAAGTTGGACTTAAAAAAAGTCCCTCCAGAGTTCAGTGCGATCCCCAGATAA	1798
OY		1140	GCAAAATTTGGCATCTGCAAAATGATTTTGGAGTGTTCCTCCAACGACTTGGAAATTCCTCAG	1199
Db		1799	GCAAAATTTGGCATCTGCAAAATGATTTTGGAGTGTTCCTCCAACGACTTGGAAATTCCTCAG	1858
OY		1200	GCAGAGACGGTTTACTAAAAAATTTGGGAAACAAAAATTCAGGCGCTATCCACTGTATC	1259
Db		1859	GCAGAGACGGTTTACTAAAAAATTTGGGAAACAAAAATTCAGGCGCTATCCACTGTATC	1918
OY		1260	ACAGTGTCTATGAAACATATAGAGTTGGTGGAAAAAGTTTATAGATCCAAATGTTTAAATATC	1319
Db		1919	ACAGTGTCTATGAAACATATAGAGTTGGTGGAAAAAGTTTATAGATCCAAATGTTTAAATATC	1978
OY		1320	ACCCTCACTGTGGCCCGAGTTCGAGAGGAGTAGTGTTCCTGAGCTRAGCCAAATTCATAGTGC	1379
Db		1979	ACCCTCACTGTGGCCCGAGTTCGAGAGGAGTAGTGTTCCTGAGCTRAGCCAAATTCATAGTGC	2038
OY		1380	TCCCTTTTGATGTGCGAGATTATATCTGATTTTAAAGAAAGTATGTCGACAAAATCTACA	1439
Db		2039	TCCCTTTTGATGTGCGAGATTATATCTGATTTTAAAGAAAGTATGTCGACAAAATCTACA	2098
OY		1440	ATATTTCTATGAAACATTCACAGGAAATGGAAGACATACAGTTTATCATTTGATTCACCTT	1499
Db		2099	GTATTTCTATGAAACATTCACAGGAAATGGAAGACATACAGTTTATCATTTGATTCACCTT	2158
OY		1500	TTTCTGTGAGTAAAAAATTTTACAGAATTTGCTTCCAGTTTCAGGGAAGAGCTCCAGAGACT	1559
Db		2159	TTTCTGTGAGTAAAAAATTTTACAGAATTTGCTTCCAGTTTCAGGGAAGAGCTCCAGAGACT	2218
OY		1560	TTGCACAAACCAACCCCAATATTGTTTAAGAATGATGATGATCAACATCATGTCTTGAGAA	1619
Db		2219	TTGCACAAACCAACCCCAATAGTATTAAAGATGATGATGATCAACATCATGTCTTGAGAA	2278
OY		1620	GAGCATTATTTGATCATTTAAGGTTTACACAGACAGACCTTTTATAGGCATGTCAATATG	1679
Db		2279	GAGCATTATTTGATCATTTAAGGTTTACACAGACAGACCTTTTATAGGCATGTCAATATG	2338
OY		1680	CTCCAACACGCCACCAAAAGTATGCGAAGGAGTATTTCCACAGGAATTTATGATGCTCTGT	1739
Db		2339	CTCCAACACGCCACCAAAAGTATGCGAAGGAGTATTTCCACAGGAATTTATGATGCTCTGT	2398
OY		1740	TTGATATTGGAAGCAAAAGTGGACCTTCCAAAGGCTGGGAGATGTAAGAAGACAGATTT	1799
Db		2399	TTGATATTGGAAGCAAAAGTGGACCTTCCAAAGGCTGGGAGATGTAAGAAGACAGATTT	2458
OY		1800	CTGTGTGACGCTTCACAGTGCAGGCACTGCAGAGACTTTGAGTGAAGTACGCTTAAGAGG	1859
Db		2459	ATGTTTGCAGGCTTCACAGTGCAGGCACTGCAGAGACTTTGAGTGAAGTACGCTTAAGAGG	2518
OY		1860	ATTCTTTAGAGACCTGCTATTTGAATTTGTGTGATCTCACTC--AAAAGATATATATG	1917
Db		2519	ATTCTTTAGAGAACTCGTATTTGAATTTGTGTGATCTCACTCAGAAAGATCGTAATG	2578
OY		1918	GTAATATTGATAAATTTTAAAAATTGTAATTTGTAATTAAGTAAGTGTGAATATATATATATAA	1977
Db		2579	GTAATATTGATAAATTTTAAAAATTGTAATTTGTAATTAAGTAAGTGTGAATATATATATATAA	2638
OY		1978	AAAAAAAAAAAAAAAA 1992	
Db		2639	AAAAAAAAAAAAAAAA 2653	
RESULT 4				
LOCUS	123794	123794	2653 bp DNA linear PAT 07-Oct-1996	

DEFINITION	Sequence 1 from patent US 5538866.
ACCESSION	123794
VERSION	123794.1 GI:1603664
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 2653)
TITLE	Israel, R.S., Heston, W.D.W. and Fair, W.R.
JOURNAL	Prostate-specific membrane antigen
FEATURES	Patent: US 5538866-A 1 23-JUL-1996;
	Location/Qualifiers
	1..2653
BASE COUNT	782 a 524 c 640 g 707 t
ORIGIN	
Query Match	85.5%; Score 1702.6; DB 6; Length 2653;
Best Local Similarity	98.5%; Pred. No. 0;
Matches 1729;	Conservative 0; Mismatches 24; Indels 2; Gaps 1;
QY	240 AGGTTAAAGATGCCAGCTGGCAGGGGCCAAAGAGATCTCTACTCAGACCCCTGCTG 299
DB	
	899 AGGTTAAAGATGCCAGCTGGCAGGGGCCAAAGAGATCTCTACTCAGACCCCTGCTG 958
QY	300 ACTACTTGGCTCCTGGGGGGAAGTCTCTATCCAGAGGTGGAAATCTCTGGAGAGTGGT 359
DB	
	959 ACTACTTGGCTCCTGGGGGGAAGTCTCTATCCAGAGGTGGAAATCTCTGGAGAGTGGT 1018
QY	360 TCCAGCGTGGAAATATCTCTAAATCTGAATGTGTGACAGAGACCCCTCTCAGCCAGTTACC 419
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DB	
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DB	
	1619 ACTCATCTATAGAAGAACTACACTGTAGAGTTGATTTGACACCACTGATGTACAGCT 1678

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QY	1140	GCAAAATGGGATCTGCAATGATTTTGGAGTGTTCCTCCACAGACTTGAATTGCTTCAG	1199
Db	1799	GCAAAATGGGATCTGCAATGATTTTGGAGTGTTCCTCCACAGACTTGAATTGCTTCAG	1858
QY	1200	GCAGAGCAGGTTATCTAAAAAAATTGGGAAACAAACAAATTCAGGGGTATCCACTGTATC	1259
Db	1859	GCAGAGCAGGTTATCTAAAAAAATTGGGAAACAAACAAATTCAGGGGTATCCACTGTATC	1918
QY	1260	ACAGTGTCTATGAAACATATAGAGTTGGTGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1319
Db	1919	ACAGTGTCTATGAAACATATAGAGTTGGTGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1978
QY	1320	ACCTCACTGTGGCCCGCAGGTTCCAGAGGAGATGCTGTTTGAGCTAAGCAATTCATAGTGC	1379
Db	1979	ACCTCACTGTGGCCCGCAGGTTCCAGAGGAGATGCTGTTTGAGCTAAGCAATTCATAGTGC	2038
QY	1380	TCCCTTTTGATGTGCGAGATTATGCTGTAGTTTAAAGAAATGATGCGACAAAATCTACA	1439
Db	2039	TCCCTTTTGATGTGCGAGATTATGCTGTAGTTTAAAGAAATGATGCGACAAAATCTACA	2098
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Db	2099	GTATTTCTATGAAACATCTCCACAGAAATGAAGCATACAGTTTATCATTTGATTCACCTTT	2158
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Db	2159	TTTCTGCAGTAAAAATTTTACAGAAATGCTTCCAAAGTTCCAGGAGACACTCCAGACT	2218
QY	1560	TTGCAAAAGAACCCCAATATGTTAAGAAATGAAATGATCAATCACTATGTTCTGGAAA	1619
Db	2219	TTGCAAAAGAACCCCAATATGTTAAGAAATGAAATGATCAATCACTATGTTCTGGAAA	2278
QY	1620	GAGATTATTTGATTCACATTAGGGTTTACACAGACACTTTTATAGGCATGTCACTATG	1679
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QY	1680	CTCCACAGCAGCACACAGATATGCGAGGGAGTCATTTCCAGGAATTTATGATGCTCTGT	1739
Db	2339	CTCCACAGCAGCACACAGATATGCGAGGGAGTCATTTCCAGGAATTTATGATGCTCTGT	2398
QY	1740	TTTGATTTGGAAGCAAGTGGACCTTCCAGGCGCTGGGGAGATGTGAAGAGACAGANTTT	1799
Db	2399	TTTGATTTGGAAGCAAGTGGACCTTCCAGGCGCTGGGGAGATGTGAAGAGACAGANTTT	2458
QY	1800	CTGATTGCAGCTTTCACAGTGCAGCAGCTGCAGAGACTTTAGTGAAGTACCTTAAGAG	1859
Db	2459	ATGTTGCAAGCTTTCACAGTGCAGCAGCTGCAGAGACTTTAGTGAAGTACCTTAAGAG	2518
QY	1860	ATTCCTTGAAGACTCTGTATTGAATTTGTGTGATGTCACTC--AAAGAAATAATATGG	1917
Db	2519	ATTCCTTGAAGAAATCCGATATGAATTTGTGTGATGTCACTCAGAAAGAAATCGTAATGG	2578
QY	1918	GTATATTTGATTAATTTTAAATTTGGTATATTGGAATTAAGTTGAATTTTATATATAAA	1977
Db	2579	GTATATTTGATTAATTTTAAATTTGGTATATTGGAATTAAGTTGAATTTTATATATAAA	2638
QY	1978	AAAAAAAAAAAAAAAAA 1992	
Db	2639	AAAAAAAAAAAAAAAAA 2653	

Accession	Version	Keywords	Source	Organism	Reference Authors Title	Journal MEDLINE PubMed Comment
M99487	GI:190663	prostate-specific membrane antigen.	Homo sapiens (human)	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
1	(bases 1 to 2653)				Israeli,R.S., Powell,C.T., Fair,W.R. and Heslon,W.D. Molecular cloning of a complementary DNA encoding a prostate-specific membrane antigen Cancer Res. 53 (2), 227-230 (1993)	
Original source text:						Original source text: Homo sapiens (tissue library: LNCap CDNA of Ron Israeli) male prostatic carcinoma metastatic lymph node CDNA to mRNA.
FEATURES	source	Location/Qualifiers				
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		/translation="MNVLHETDQAVATARPRLVAGALVLAGFFELGLFGFMFLIKSSNENATITPKHNKAKFLIDELKAENIKPLYNFOIHLGETEONFOLAKIOSOMKEFGADSVLAHYDLVLSPTKTHPIYISINDGMEIFNTSLPFPPEGYENVSDIVPPESAFSPQGMPEGDLVYNVAATEDFEFLERDMKINCSGKIYIAIKGVFRKNRKNNQLAGKAGVILSDPADYPAPGVYSDDAKMLPEGVGNGNLINLGADDPITPGIPANEYAYRGJAEANVGLPSIIVPHIGYDAOKMLEKMGSAAPPSSMGSLKVPVNWGEFTLNSTOKRVKMHISTNEVTIRIYVIGTLRGAVEDRYVILGGHRDSWVFGLIDPOSGAAYVEIYRSFGTLTKEGMRPRRTLLPASMDAEEBGLGSTEMAEENSLSLOEBGVAVMABDSICGNLTTRLDCTPLMTSLVHNLTLEKSPDGPECKSLYESWTNRKSPPSEFSMPRIKSLUGSGDEVEVFQRLGIASGRARITKNMETNKFSGTPLYHSYIEIYEKPYDPMKKHLTAOVGGMVFEELANSIVLPEDCRDAVVLRKYADKIYISIMKHPEMKTYVSFDLSFAVNKETEIASKFSERLDQFNPNIVLRMMNDLMFLERATIDLGLGLDRPYRHVIYAPSSSHNNKYAGESPFIYDALFDIESKVDPSKAMEGVKROIYVAFTVQAAMETLSEVA"				
BASE COUNT	782 a	524 c	640 g	707 t		
ORIGIN						
Query Match	85.5%	Score 1702.6;	DB 9;	Length 2653;		
Best Local Similarity	98.5%;	Pred. No. 0;				
Matches 1729;	Conservative	0;	Mismatches 24;	Indels 2;	Gaps 1;	
Oy.	240 AGGTAAAAATGCCACGCTGGCAGGGCGCAAGAAGATCTCTACTCAGACCCTGCTG	299				
Dd	899 AGGTAAAATAATGCCACGCTGGCAGGGCGCAAGAAGATCTCTACTCAGACCCTGCTG	958				
Oy	300 ACTACTTGTCCTCGGGGTGAAGTCTTATCCAGACGGTTGGAAATCTTCTGGAGGTGGTG	359				
Dd	959 ACTACTTGTCCTCGGGGTGAAGTCTTATCCAGACGGTTGGAAATCTTCTGGAGGTGGTG	1018				
Oy	360 TCCAGCGCGGAAATATCTTAATCATGCATGGTGGCAGGAGACCTCTCACACAGGTATCC	419				
Dd	1019 TCCAGCGCGGAAATATCTTAATCATGCATGGTGGCAGGAGACCTCTCACACAGGTATCC	1078				
Oy	420 CAGCAAAATGATACGCTTATAGGATGGAATTGCGAGAGCTGTGGTCTTCCAACTATTC	479				
Dd	1079 CAGCAAAATGATATGCTTATAGGCTCGGAATTGCGAGAGCGTGTGGTCTTCCAACTATTC	1130				

OY	480	CTGTTTCATCCAGTGGATGACTAATGTGCACAGAAAGCTCCTAAGAAAAATGGGTGGCTCAG	539
Dd	1139	CTGTTTCATCCAAATTGGATACATAATGTGCACAGAAAGCTCCTAAGAAAAATGGGTGGCTCAG	1198
OY	540	CACCACCGAGTAGCAGGCTGGAGAGGAAGCTCAAAAGTGCTCCATCAATGTTGGACCTGGCT	599
Dd	1139	CACCACCGAGTAGCAGGCTGGAGAGGAAGTAATCTCAAAGTGCTCCATCAATGTTGGACCTGGCT	1258
OY	600	TTACTGSAAGCTTTTCTACACAAAAAGTCAAGATATGCACATCCACATCTACCAATGAAGTGA	659
Dd	1259	TTACTGSAAGCTTTTCTACACAAAAAGTCAAGATATGCACATCCACATCTACCAATGAAGTGA	1318
OY	660	CGAGAATTTCACAATGTGATAGGTACTCTCAGAGAGCAGTGGAAACACAGACAGATATGTCA	719
Dd	1319	CAAGAAATTTACAATGTGATAGGTACTCTCAGAGAGCAGTGGAAACACAGACAGATATGTCA	1378
OY	720	TTCTGGAGAGTCCACCGGAGCTCATGGGTGTTGGGTATTTAGCCCTCAGAGTGGAGAG	779
Dd	1379	TTCTGGAGAGTCCACCGGAGCTCATGGGTGTTGGGTATTTAGCCCTCAGAGTGGAGAG	1438
OY	780	CTGTTGTTTCATGAACCTGTGAGGAGCTTTGGAACATGATAAAAAGGAAGGTGGAGACCTA	839
Dd	1439	CTGTTGTTTCATGAACAAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGTGGAGACCTA	1498
OY	840	GAGAACAAATTTGTTTGCAGCTGGGATGCGAGAAGAAFTTGGTCTCTGTTGGTCTACTG	899
Dd	1499	GAGAACAAATTTGTTTGCAGCTGGGATGCGAGAAGAAFTTGGTCTCTGTTGGTCTACTG	1558
OY	900	AGTGGGCGAGAGTAATTCAGAGACTCCTTCAAGACCGTGGGTGGCTTATATTAATGCTG	959
Dd	1559	AGTGGGCGAGAGAGTAATTCAGAGACTCCTTCAAGACCGTGGGTGGCTTATATTAATGCTG	1618
OY	960	ACTCATCTATGGAAGGAACCTACACTCTGGAAGTGTGATTTACACACACTGATGTACACT	1019
Dd	1619	ACTCATCTATGGAAGGAACCTACACTCTGGAAGTGTGATTTACACACCGCTGATGTACACT	1678
OY	1020	TGCTATACAACTTAACAAAGAGGTGAAGAAACCCGTATGAGAGGCTTTGAAGCAAAATCTC	1079
Dd	1679	TGCTATACAACTTAACAAAGAGGTGAAGAAACCCGTATGAGAGGCTTTGAAGCAAAATCTC	1738
OY	1080	TTTTATGAAGTTGGACATRAAAAAAGTCTTCCCAGAGTTCAGTGGCATGCCAGAGATTA	1139
Dd	1739	TTTTATGAAGTTGGACATRAAAAAAGTCTTCCCAGAGTTCAGTGGCATGCCAGAGATTA	1798
OY	1140	GCAAATTTGGAGTCTGGAAATGATTTTGGAGGTCTTCCAAGCAAGCTTGGAAATGCTTCAG	1199
Dd	1799	GCAAATTTGGAGTCTGGAAATGATTTTGGAGGTCTTCCAAGCAAGCTTGGAAATGCTTCAG	1858
OY	1200	GCAGAGCACGGTATACTRAAAAAATTGGGAACAAACAAATTCAGCGGCTATCCACTGTATC	1259
Dd	1859	GCAGAGCACGGTATACTRAAAAAATTGGGAACAAACAAATTCAGCGGCTATCCACTGTATC	1918
OY	1260	ACAGTGTCTATGAAGAAATANTAGTGTGGTGGAAAAAGTTTATGATCCATGTTTAAATATC	1319
Dd	1919	ACAGTGTCTATGAAGAAATANTAGTGTGGTGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1978
OY	1320	ACCTCAGTGTGGCCAGGTTGAGAGAGGGAATGATGTTGACCTAGGCCAATTCATATAGTC	1379
Dd	1979	ACCTCAGTGTGGCCAGGTTGAGAGAGGGAATGATGTTGACCTAGGCCAATTCATATAGTC	2038
OY	1380	TTCCCTTTTGATTTGTCGAGATTAATGCTGTAGTTTAAAGAAATATGTCGACAAATCTTACA	1439
Dd	2039	TTCCCTTTTGATTTGTCGAGATTAATGCTGTAGTTTAAAGAAATATGTCGACAAATCTTACA	2098
OY	1440	ATATTTTCATGAACATCCACAGAAATGAAGACATACAGTTTATPCATTTATTCACATT	1499
Dd	2099	ATATTTTCATGAACATCCACAGAAATGAAGACATACAGTTTATPCATTTATTCACATT	2158
OY	1500	TTTCTGCAGTAAAAAATTTTACAGAAATGCTTCCAAAGTTACGAGAGACTCCAGAGACT	1559
Dd	2159	TTTCTGCAGTAAAAAATTTTACAGAAATGCTTCCAAAGTTACGAGAGACTCCAGAGACT	2218

QY	1560	TTGACAAAGAACCACCATATTGTTAACAATGATGAATGATCACTATGTTTCTGGAAA	16119
Db	2219	TTGACAAAGAACCACCATATTGTTAACAATGATGAATGATCACTATGTTTCTGGAAA	2278
QY	1620	GAGCATTTATTTGATTCATTAGGGTTACAGACAGACCTTTTATATGGCATGTCACTATG	1679
Db	2279	GAGCATTTATTTGATTCATTAGGGTTACAGACAGACCTTTTATATGGCATGTCACTATG	2338
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Db	2399	TTGATATTGAAAGCAAAAGTGGACCCCTTCACAAAGCCCTGGGGAGATGTGAAGACAGATT	2458
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QY	1860	ATTTCTTTAGAGACTTCGTATTTGAATTTGTGTGATGTGCACCTC--AAAGATAATTAATG	1917
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QY	1918	GTATATTGATTAATTTTAAATTTGGTATATTGGAATTAAGTTGAATTTATATATAAAA	1977
Db	2579	GTATATTGATTAATTTTAAATTTGGTATATTGGAATTAAGTTGAATTTATATATAAAA	2638
QY	1978	AAAAAAAAAAAAAAAA 1992	
Db	2639	AAAAAAAAAAAAAAAA 2653	
RESULT 6			
AF176574			
LOCUS	AF176574	2518 bp	mRNA
DEFINITION	Homo sapiens folylipoly- γ -glutamate carboxypeptidase (FCGP)	linear	PRI 28-NOV-2000
ACCESSION	AF176574		
VERSION	AF176574.1		
KEYWORDS	GI:5762481		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 2518)		
AUTHORS	Devlin,A.M., Ling,E.H., Pearson,J.M., Fernando,S., Clarke,R., Smith,A.D. and Halsted,C.H.		
TITLE	Glutamate carboxypeptidase II: a polymorphism associated with lower levels of serum folate and hyperhomocysteinemia		
JOURNAL	Hum. Mol. Genet. 9 (19), 2837-2844 (2000)		
PUBLISHED	Hum. Mol. Genet. 9 (19), 2837-2844 (2000)		
REFERENCE	2 (bases 1 to 2518)		
AUTHORS	Devlin,A.M., Ling,E.-H. and Halsted,C.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-AUG-1999) Internal Medicine, University of California, Davis, TB 156, Davis, CA 95616, USA		
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 F G L S D P E M E L H D V L S T P A N T H A R E N I T S I L I N E G N E K I N F E N T S I E P P P E V E N S I O V P P
 F S A S P O G M E G L A D V Y N N A R E A D F E K R E D L K I N S C S I Y A R G A Y E K R N A K M A O
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 Y A R R G I A E A N G P I D P V H I G Y D K A D L I E M G S A P D S S M R L K V P P A N V G A E T F
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 A A A E T L E S E V A

BASE COUNT	747 a	491 c	604 g	676 t
ORIGIN				

Query Match	84.9%	Score 1690.6;	DB 9;	Length 2518;
Best Local Similarity	98.5%	Pred. No. 0;		
Matches 1717; Conservative	0;	Mismatches 24;	Indels 2;	Gaps 1;

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QY	300	ACTACTTTCCTCCTGGGGGTGAAGTCCATCCAGACGGCTTGGAAATCTTCCCTGGAGAGTGTG	359
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QY	420	CAGCAAAATGATATACGCTTATATAGCATGGAATTTGACAGAGCGTTGGTCCCTCCAAAGTATTC	479
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QY	480	CTGTTTCATCCAGTTGGATCTATGATATCATGCACAGAAAGCTCTAGAAAAAATGGGTGGCTCAG	539
Db	1016	CTGTTTCATCCAAATTTGGATCTATGATATCATGCACAGAAAGCTCTAGAAAAAATGGGTGGCTCAG	1075
QY	540	CACACACAGATATAGAGCGTGGAGAGAGTCCAAAGTGTCTCTACAAATGGTGGACCTGGCT	599
Db	1076	CACACACAGATATAGAGCGTGGAGAGAGTCCAAAGTGTCTCTACAAATGGTGGACCTGGCT	1135
QY	600	TTACTGGAAATCTTTCTACACAAAAAGTCAAGATGACATCCACTCTACCAATTAAGTGA	659
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QY	780	CTGTTGTTTCATGAAGAACTGTGAGAGCTTTGGAACTGAAAAAGAGGGGTGAGACCTTA	839
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QY	840	GAAGAACAATTTTGTTCGCAAGCTGGGATGCGAGAGAAATTTGTCTTCTTGGTCTTACTG	899
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Db	1436	AGTGGGCGAGAGAAATTTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATTTAATGCTG	1495
QY	960	ACTCATCTATGAGAGAAACTACACTCTGAGAGTGTGATTTGACACCACTGATGTACAGCT	1019
Db	1496	ACTCATCTATGAGAGAAACTACACTCTGAGAGTGTGATTTGACACCGCTGATGTACAGCT	1555
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Qy	1320	ACCTCAGCTGTGGCCAGGTTGAGAGAGGAGTGTGTTGAGCTAGCCAAATTCATAGTGC	1379
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Qy	1740	TTGATATTTGAAGCAAATGTGACCCCTTCCAGAGCCTGGGAGATGCAAGACAGATTT	1799
Db	2276	TTGATATTTGAAGCAAATGTGACCCCTTCCAGAGCCTGGGAGATGCAAGACAGATTT	2335
Qy	1800	CTGTTGACGCTTCCACAGTCGACGACGCTGCAGAGACTTTGATGTAAGTATGACTATAGAG	1859
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Qy	1860	ATTCCTTATGACACTCTGATGTAATTTGTGTGATGTGCACTC--AAAGATTAATTAAGG	1917
Db	2396	ATTCCTTATGACACTCTGATGTAATTTGTGTGATGTGCACTCAGAAAGAAATCGTAATGG	2455
Qy	1918	GTAATTTGATTAATTTTAAAAATTTGGTATATTTGAAATTAAGTTGAAATTTATATATAAA	1977
Db	2456	GTAATTTGATTAATTTTAAAAATTTGGTATATTTGAAATTAAGTTGAAATTTATATATAAA	2515
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RESULT 7	AX376036	LOCUS	AX376036	2558 bp	DNA	linear	PAT 01-MAR-2002
DEFINITION	Sequence	103	from Patent WO0168848.				
ACCESSION	AX376036						

VERSION AX376036.1 GI:19170410
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L., Pan, J., Smith, Y., Watanabe, C.K., Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0168848-A 103 20-SEP-2001;
Genentech, Inc. (US)
FEATURES
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BASE COUNT 745 a 509 c 623 g 681 t
ORIGIN
Query Match 84.7%; Score 1687.2; DB 6; Length 2558;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;
QY 240 AGGTTAAATGCGCCAGCTGGCGAGGGGCCAAGAGGACATCTCTACTCAGACCCGCTG 299
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QY 360 TCCAGCGTGAATATCTTAATCTGAATGTCGAGAGACCCCTTCACACCAAGTTACC 419
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DB 1001 CACCAATGAATGCGTTATAGGATGGAATGCAAGGCTGTGGTCTTCCAAATATTC 1060
QY 480 CTGTTATCAGTGGATATGATGACAGAGCTCTAGAAAAATGGTGGCTCAG 539
DB 1061 CTGTTATCAGTGGATATGATGACAGAGCTCTAGAAAAATGGTGGCTCAG 1120
QY 540 CACCCACAGTACAGCTGGAGAGAGTCTCAAAGTCTCTCAATGTTGACCTGGCT 599
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QY 660 CGAAGATTTACAATGATAGTACTCTCAGAGAGCAGTGAAGCAGACAGATATGTCA 719
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DB 1301 TTCTGGAGAGTACCCGGGACTCATGGGTGTTGGTATTTGACCTCAAGTGGAGCAG 1360
QY 780 CTGTTGTCATGAACCTGTGAGAGCTTTGGAACACTGAAGAGGAGGTTGAGAGCTTA 839
DB 1361 CTGTTGTCATGAACCTGTGAGAGCTTTGGAACACTGAAGAGGAGGTTGAGAGCTTA 1420
QY 840 GAAGAACAAATTTGTTGCAAGCTGGATGCGAAGAAATTTGGTCTTCTGTTCTACTG 899
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DB 2021 ATATTTCTATGAACATCCACAGGAATGAAGCATACAGTTTATCATTTGATTCCTT 2080
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QY 1918 GTATATTTGAATTTTAAATTTGATATTTGAATTTGAATTTGAATTTGAATTTGAAT 1975
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RESULT 8
AX467227
LOCUS AX467227 2253 bp DNA linear PAT 16-JUL-2002

DEFINITION	Sequence 1 from Patent WO0234287.
ACCESSION	AX467227
VERSION	AX467227.1 GI:21900509
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 Beier, A.M., Gautam, A. and Mouritsen, S.R. Novel therapeutic vaccine formulations Patent: WO 0234287-A 1 02-MAY-2002;
AUTHORS	Pharmexa A/S (DK)
JOURNAL	location/Qualifiers
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Query Match	79.5%; Score 1584; DB 6; Length 2253;
Best Local Similarity	98.8%; Pred. No. 0;
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Qy	780	CTGTGTCATGAAACGTGAGAGCTTGGAAACGTGAAAGAGAGGGTGGAGACTA	839
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Db	1418	TGATATCAACCTTAACAAAGAGCTGAAAGCCCTGATGAAGCGTTTGAAGGCATAATCTC	1477
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Db	2018	GAGCATTTATGATCATTTAGAGTTACACAGACACCTTTTATAGCATGTCACTATG	2077
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Db 1778 TCCCTTTGATGTCGAGATTATGCTGATGTTTAAAGAAAGTATGTCGACAAAATCTACA 1837
 Qy 1440 ATATTTCATGAAACATCCACAGAAATGAAGACATACAGTTTATCATTTTCATCTT 1499
 Db 1838 GTATTTCATGAAATATCCACAGAAATGAAGACATACAGTTTATCATTTTCATCTT 1897
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 Qy 1560 TTGCAAAAAGCAACCCATATGTTAAGAAATGAATGATCACTGTTTCGAAA 1619
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 Db 2018 GAGCATTTATGATTCATTAGGAGTTACAGACAGACCTTTTATAGCATGTCATCTATG 2077
 Qy 1680 CTCACAGACGCCACAAAGATGACAGGGAGTCAATTCACAGAAATTTATGATGCTCTGT 1739
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RESULT 10 BC025672 LOCUS

DEFINITION Homo sapiens, similar to folate hydrolase (prostate-specific membrane antigen) 1, clone MGC:34488 IMAGE:5202715, mRNA, complete cds

ACCESSION BC025672
 VERSION BC025672.1 GI:19343603
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabs-rt@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland.
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@ncl.nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, O.L., Mastello, C., Mastian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantirip, S., Thomas, P.J., Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAX Plate: 49 Row: e Column: 5

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4758397.
 Location/Qualifiers
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 Qy 300 ACTACTTTCCTCTGGGCTGAAGTCTTCCAGACGTTTGAATTTCTCTGAGGTG 359
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 Db 1037 CTGTTTCATCCAGTTTGATATGATGTCACAGAACTCTTGAATAATGGTGGCTAG 1096
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 Db 1097 CACACAGATAGACGTCGAGAGGAATCTCAAAAGTCTCTACATGTTGGACTGGCT 1156
 Qy 600 TTACTGAAACTTTTCTACAAAAAAGTCAAGATGCACATCCATCAATGAATGTA 659
 Db 1157 TTACTGAAACTTTTCTACAAAAAAGTCAAGATGCACATCCATCAATGAATGTA 1216
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 Db 1217 CAAGATTTAATGATGATAGTACTCTCAAGAGAGCGATGGAACCAACAGATATGCA 1276
 Qy 720 TTCTGGAGGTCACCGGAGCTCATGGGTTTGGTGAATGACCTCAGAGTGAGGAG 779
 Db 1277 TTCTGGAGGTCACCGGAGCTCATGGGTTTGGTGAATGACCTCAGAGTGAGGAG 1336

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OY	840	GAAGAACAAATTTGTTTGGCAAGCTGTGGAGTGCAGAGAAATTTTGGTCTTCTTGTTGTTCTACTGT	899
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OY	960	ACATCATCTATGAAGAGAACTACACTCTGAGAGTTGATTGTATACACCATGTATGTATACACT	1019
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Db	1997	GTATTTTCTATGAAGAAATCTCACAGAGAAATGAAGACATACAGTTTATCTCAATTTATTCACATT	2056
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Db	2204	TTGATATTTGAAGCAAGTGTGACCTTCCAAAGGCTGTGGGAGATGTGAAGAGACAGATTT	2263
OY	1800	CTGTGTGACGCTTACAGCTGTGAGGCACTGTGAGAGACTTTTGAATGAAGATAGCCTTAACAGG	1859
Db	2264	ATGTTTGAAGCTTTCACAGTGTGAGGCACTGTGAGAGACTTTTGAATGAAGATAGCCTTAACAGG	2323

OY		1860	ATCTTTGAGACCTGTGATTGAATTTGTGGTGTGCACGC--AAAGAATAAATG	1917
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DEFINITION	Sequence 2 from Patent WO0226984.			
ACCESSION	AX403107			
VERSION	AX403107.1	GI:21388049		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
TITLE	Rhodes, K., Betty, M., Ling, H.P. and An, W.			
JOURNAL	Potassium channel interactors and uses therefor			
	Patent: WO 0226984-A 2 04-APR-2002;			
	Millennium Pharmaceuticals, Inc. (US)			
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Matches 1523; Conservative	0; Mismatches 6;			
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OY		360	TTCAGCGGTGAATAATCTTAATGTGATGTGGCAGGAGACCCCTCACACCAAGTTACC	419
Db		650	TTCAGCGGTGAATAATCTTAATGTGATGTGGCAGGAGACCCCTCACACCAAGTTACC	709
OY		420	CAGCAAAATGAATAGCTTATATAGGATGAATTCAGAGAGCTGTGGTCTTCCAAGTATTC	479
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 ACCESSION U75973
 VERSION U75973.1 GI:1661226
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 Rattus.
 REFERENCE 1 (bases 1 to 2899)
 AUTHORS Bzdoga,T., Turi,T., Wroblewska,B., She,D., Chung,H.S., Kim,H. and
 Neale,J.H.
 TITLE Molecular cloning of a peptidase against N-acetylserine19lutamate
 from a rat hippocampal cDNA library
 JOURNAL J. Neurochem. 69 (6), 2270-2277 (1997)
 MEDLINE 98041505
 PUBMED 9373657
 REFERENCE 2 (bases 1 to 2899)
 AUTHORS Bzdoga,T., Turi,T., Wroblewska,B., She,D. and Neale,J.H.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-1996) Biology, Georgetown University, 37th & O
 St. NW, Washington, DC 20057, USA
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Query Match	63.4%	Score 1263.6;	DB 10;	Length 2899;
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QY	420	CAGCAAAATGATATGCGCTTATATAGCATGGAAATTCGAGAGCGTGGTGGTTCTTCCAGTATTC	479	
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D	b		1326	AGTGGCAGAGGAAACATTCAAGACTCTTACAGAGAGCTGGTGTGGCTTATATCAAGCTG	1385
Q	y		960	ACTCATCTATGAAAGAAACTACTCTGAGAGTTGATTGTACACCATATGTACAGCT	1019
D	b		1386	ATTCTTCATGAGAGAAACTACTACTCTCAGAGTTGATTGTACACACCATATGACAGCT	1445
Q	y		1020	TGCTATACAACTTAACAAAGAGCTGAAAAGCCCTGATGAAAGGCTTTGAAGGCAAACTC	1079
D	b		1446	TAGATATACAACTTAACAAAGAGCTGCAACCCCGGATGAAAGGCTTTGAAGGCAAACTC	1505
Q	y		1080	TTTATGAAAGTTGAGACTTAAAGAAAGTCCCTCCAGAGTTCAGTGGCATGCCAGATAA	1139
D	b		1506	TTTATGACAGCTGGAAAGAAAAAGTCCCTTCACTGATGATTCATTGGAAATGCCAAGATTA	1565
Q	y		1140	GCAAAATGGAGCTGGAATGATTTTGAAGTGTCTTCCAAAGCATTTGGAATTCCTTCA	1199
D	b		1566	GCAAGCTGGGGCTGGCAATGATTTTGAAGTGTCTTCCAAAGCATTTGGAATTCCTTCA	1625
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Q	y		1320	ACCTCAGTGTGGCCAGGTTGAGAGAGGATGTGTGTTGAGCTAGCCAAATTCATATGC	1379
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Q	y		1380	TCCCTTTGATTTGTCGANAATTATGCTGTAGTTTAAAGAAAGTATGCGACAAATTCACA	1439
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Q	y		1440	ATATTTCTATGAAACATCCACAGGAAATGAAAGATACAGTTATCTATCTTATTCACCTT	1499
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D	b		1926	TTTTTGCACTAAAAAATTTTACAGATGTTGTCATCCCAAGTCTCAACAGAGAGCTGCAAGCT	1985
Q	y		1560	TTGACAAAGCAACCCAAATTTGTTAAGAAATGAATGAATCACTATGTTTGTGGAAA	1619
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Q	y		1620	GAGCATTTATTTAGCATTTAGGGTTACAGACAGACCTTTTATAGGATCTCATATG	1679
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Q	y		1740	TTGATATTTGAAGCAAAAGTGAACCTTCCCAAGGCTTGGGGAGTGTGAAGAGACAGATT	1799
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Q	y		1800	CTGTTGACGCTTCCACAGTGCAGAGAGCTGCAGAGACTTTAGTGAATACCTTAAGAG	1859
D	b		2226	CTATTGCAAGCTTCCACAGTGCAGAGCTGCAGAGAGACTCTAGAGAAATACACTTAAGAG	2285
Q	y		1860	ATTCTTTAGAGACTCTGTATTTGAATTTGTGTGTATGTCACTCAAGAATATATAGGT	1919
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Q	y		1920	ATATTTGATTAATTTTAAAAATTTGGTATATTTGAATTAAGTTGAATTTATTTAAAAAA	1979
D	b		2342	TTCATTAATGACTTAATTTTGGCATGTATTACTAATAAATTTTAAAAATTCATATGATTTAA	2401
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[illegible]

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OY	480	CTGTTCATCCAGTTGGATACATATGATGTCACAGAAAGCTCTTGAAAAAATGGGTGGCTCAG	539
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OY	540	CACCACCGATATGACGCTGGAGAGGAATCTCAAAAGTGTCTTACAAATTTGGACTGTGCT	599
Db	1015	CACCCCTCGACAGCAGCTGGAGAGGAGACCTAAAGATGCCCTTTACAAACGTGGACCTGGCT	1074
OY	600	TTACTCGAAACCTTTTCTACAAAAAAGTCAAGATATGCATATCCATCTCCCAATGAAAGTA	659
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Db	1255	CTGTGTTCATGAAGAAATTTGTCAAGGACTTTTGGAACTCTGAAGAGAAAGGTTGGAGGCTTA	1314
OY	840	GAAGAAACAAATTTGTTTGCAAGCTGGGATGACAGAAATTTGGTCTTCTTGGTCTTACTG	899
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OY	1320	ACCTTCACGTGGCCAGGTTGAGAGAGGATGTGTGTTGACTATGCCAATTCATATGTC	1379
Db	1795	ACCTTCACGTGGCCAGGTTGAGAGAGCAATGTGTTTGAATTTGGCCAAATTCATATGTC	1854
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RESULT 15
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LOCUS AF513486
DEFINITION Rattus norvegicus N-acetylated alpha-linked acidic dipeptidase
(Naalad) mRNA, complete cds.
ACCESSION AF513486
VERSION AF513486.1 GI:21314595
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2259)
AUTHORS Park, S.Y. and Lee, W.
TITLE Direct Submission
JOURNALS Submitted (18-MAY-2002) Department of Biochemistry, School of
Medicine, Dongguk University, 707 Suk-dang Dong, Kyungju, Kyung-Buk
780-714, Korea
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ORIGIN
Query Match 63.0%; Score 1254.4; DB 10; Length 2259;
Best Local Similarity 86.0%; Pred. No. 9.8e-277;
Matches 1390; Conservative 0; Mismatches 226; Indels 0; Gaps 0;
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OY 660 CGAGAATTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 719
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Db 1124 TTCTGGAGGTCACCGGAGCTCATGGGCTTGGTATGATGATGATGATGATGATGATGATG 1183
OY 780 CTGTTGTTCAATGAACTGTGAGAGCTTTGGAACTGAAAAGAGAGGAGTGAAGCTGA 839
Db 1184 CTGTTGTTCAATGAACTGTGAGAGCTTTGGAACTGAAAAGAGAGGAGTGAAGCTGA 1243
OY 840 GAAGAACAATTTTGTTCAGAGCTGGAGATGAGAGAAATTTGTTCTCTGTTGTTCTACTG 899
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OY 900 AGTGGCAGAGAGATTAATTAAGACTCTTCAAGAGCGCTGGGCTGTTATATTAATGCTG 959
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OY 1020 TGTATACAACTTAACAAAAGAGCTGAAAGCCCTGATGAGAGCTTTGAAAGCAATCTC 1079
Db 1424 TAGATATCAACTTAACAAAAGAGCTGAAAGCCCTGATGAGAGCTTTGAAAGCAATCTC 1483
OY 1080 TTTTATGAAAGTGGACATTAAGAAAGTCTTCCAGAGGTTGAGTGGATGCCCGAGGATA 1139
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; CLONE: Prostate-Specific Membrane Antigen
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 262..2511
; US-08-325-553-1

Query Match      85.5%; Score 1702.6; DB 1; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

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OY      300 ACTACTTGGCTCCTGGGGGTGAAGTCTTATCCAGAGGCTTGGAAATCTTCTGGAGGTG 359
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      959 ACTACTTGGCTCCTGGGGGTGAAGTCTTATCCAGATGGTTGGAATCTTCTGGAGGTG 1018
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OY      360 TCCAGCGTGGAAATATCTTAATCTGAATGTGTCAGAGAGACCTCTCACACAGGTTACC 419
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      1019 TCCAGCGTGGAAATATCTTAATCTGAATGTGTCAGAGAGACCTCTCACACAGGTTACC 1078
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OY      420 CAGCAAAATGAATACGCTTATAGCAATGTCAGAGAGGCTGTGGCTTCCAGATATTC 479
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OY      480 CTGTTTCATCCAGTTGGATCTATGATGCACAGAAAGCTCTTAGAAAAATGGGTGGCTCAG 539
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OY      540 CACCAACAGATAGACGCTGGAGAGAAAGTCTCAAGTCTCTCAAAATGTTGGACCTGGCT 599
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OY      660 CGAGAATTTACATGTGATAGTACTCTCTCAGAGAGACGTCGAAACACAGCATATGTCA 719
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OY      720 TTCTGGAGGTCACCGGACATCATGGGTTGGTGGTATGACCCCTAGAGTGGAGAG 779
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OY      780 CTGTTGTTTCATGAACTGTCAGAGGCTTTGGAAACACTGAAAAAGGAAGGTGGAGACCTA 839
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      1439 CTGTTGTTTCATGAACTGTCAGAGGCTTTGGAAACACTGAAAAAGGAAGGTGGAGACCTA 1498
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OY      840 GAAGAACATTTTGTTCGCAAGCTGGGATGCAAGAAATTTGGTCTTCTGGTTCAGTG 899
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OY      900 AGTGGCGAGAGGATTAATCAAGACTCTTCAAGAGCTGGCGTGGCTTATATTAATGCTG 959
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OY      960 ACTCATTTATAGAAAGAACTACACTCTGAGAGTTGATTTGATACACACTGATGTACAGCT 1019
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      1619 ACTCATTTATAGAAAGAACTACACTCTGAGAGTTGATTTGATACACACTGATGTACAGCT 1678
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OY      1020 TGGTATACACCTAACAAGAGAGCTGAAAAGCCCTGATGAGAGGCTTTGAAGCAATCTC 1079
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      1679 TGGTATACACCTAACAAGAGAGCTGAAAAGCCCTGATGAGAGGCTTTGAAGCAATCTC 1138
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US-08-394-152A-1
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; Patent No. 5935818
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S.
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
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STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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ORGANISM: Homo sapiens
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate-Specific Membrane Antigen
FEATURE:
NAME/KEY: CDS
LOCATION: 262..2511
US-08-394-152A-1

Query Match 85.5%; Score 1702.6; DB 2; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1739; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 240 AGGTTAAATGCCCCAGCTGCGAGGGGCCAAAGAGTCAATCTCTACTACAGACCTGCTG 299
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QY 300 ACTACTTCTCTCTGGGGTGAAGTCTATCCAGACGGTTGGAATCTTCTGAGAGTGTG 359
DB 959 ACTACTTCTCTCTGGGGTGAAGTCTATCCAGATGTGGAATCTTCTGAGAGTGTG 1018
QY 360 TCCAGCGTGAATATCTTAATCTGAATGTGAGAGAGACCTCTCACACAGGTTACC 419
DB 1019 TCCAGCGTGAATATCTTAATCTGAATGTGAGAGAGACCTCTCACACAGGTTACC 1078
QY 420 CAGCAAAATGATACGCTTATAGGCAATGCAATGCAAGAGCTTTGGTCTTCCAAAGTATTC 479
DB 1079 CAGCAAAATGATATGTTATAGGCGTGAATGCAAGAGCTTTGGTCTTCCAAAGTATTC 1138
QY 480 CTGTTTCATCCAGTGGATATCTATGATGCACAGAGCTCCTAGAAAAATGGGTGCTCAG 539
DB 1139 CTGTTTCATCCAAATGATATGATGACAGAAAGCTCTAGAAAAATGGGTGCTCAG 1198
QY 540 CACACACAGATGACGCTGAGAGAGAGTCTCAAGTGTCTACAAATGTTGACCTGGCT 599
DB 1199 CACACACAGATGACGCTGAGAGAGAGTCTCAAGTGTCTACAAATGTTGACCTGGCT 1258
QY 600 TTACTGGAATCTTTCTACACAAAAGTCAAGATGCACATCCACTCTTACCAATGAAGTA 659
DB 1259 TTACTGGAATCTTTCTACACAAAAGTCAAGATGCACATCCACTCTTACCAATGAAGTA 1318
QY 660 CGAGAAATTTACAATGATGATGATCTCTGAGAGAGACAGTGAACCAAGACAGATATGTCA 719
DB 1319 CGAGAAATTTACAATGATGATGATCTCTGAGAGAGACAGTGAACCAAGACAGATATGTCA 1378

QY 720 TTCTGGAGGTACCCGGACTCATGGGTGTTGGTGTATGACCTCAGAGTGAAGCAG 779
DB 1379 TTCTGGAGGTACCCGGACTCATGGGTGTTGGTGTATGACCTCAGAGTGAAGCAG 1438
QY 780 CTGTGTTGATGAACTGTGAGAGAGCTTTGGAACACTGAAAAAGGAGGTGAGACCTA 839
DB 1439 CTGTGTTGATGAAATTTGAGAGAGCTTTGGAACACTGAAAAAGGAGGTGAGACCTA 1498
QY 840 GAAGAAATTTTGTGTCAGAGTGGGATGACAGAAATTTGGTCTTCTTGGTCTACTG 899
DB 1499 GAAGAAATTTTGTGTCAGAGTGGGATGACAGAAATTTGGTCTTCTTGGTCTACTG 1558
QY 900 AGTGGCAGAGATTAATTAAGACTCTCCAGAGAGGTGGCGGCTTATTAATATGCTG 959
DB 1559 AGTGGCAGAGAGATTAATTAAGACTCTCCAGAGAGGTGGCGGCTTATTAATATGCTG 1618
QY 960 ACTCATCTATAGAGAAACCTACACCTGAGAGTTGATGACACCACTGATGTACAGCT 1019
DB 1619 ACTCATCTATAGAGAAACCTACACCTGAGAGTTGATGACACCACTGATGTACAGCT 1678
QY 1020 TGGTATACAACTTAACAAAAGAGCTGAAAAAGCCCTGATGAGGCTTTGAAGCAATCTC 1079
DB 1679 TGGTATACAACTTAACAAAAGAGCTGAAAAAGCCCTGATGAGGCTTTGAAGCAATCTC 1738
QY 1080 TTTATGAAGTTGGACTAAAAAAGTCTCCCAAGTTCCAGTGGCATGCCAGGATPA 1139
DB 1739 TTTATGAAGTTGGACTAAAAAAGTCTCCCAAGTTCCAGTGGCATGCCAGGATPA 1798
QY 1140 GCAAAATGGGATCTGGAATGATTTTGAAGTGTCTCCACAGACTTGAATGTCTCAG 1199
DB 1799 GCAAAATGGGATCTGGAATGATTTTGAAGTGTCTCCACAGACTTGAATGTCTCAG 1858
QY 1200 GCAGAGCAGGTAATCTAAAAATTTGGGAAACAAACAAATTCAGCGCTTTCACCTATAC 1259
DB 1859 GCAGAGCAGGTAATCTAAAAATTTGGGAAACAAACAAATTCAGCGCTTTCACCTATAC 1918
QY 1260 ACAGGTCTATGAAATCATATGAGTTGGTGAAGTTTATGATCCAAATGTTAAATATAC 1319
DB 1919 ACAGGTCTATGAAATCATATGAGTTGGTGAAGTTTATGATCCAAATGTTAAATATAC 1978
QY 1320 ACCTCAGTGGCCCGAGTTTCGAGAGGAGTGTGTTGAGTAGCCAAATTCATATGTC 1379
DB 1979 ACCTCAGTGGCCCGAGTTTCGAGAGGAGTGTGTTGAGTAGCCAAATTCATATGTC 2038
QY 1380 TCCCTTTGATGTGAGATTTATGCTGATGTTTAAAGAAATAGTGTGCAAAATCTACA 1439
DB 2039 TCCCTTTGATGTGAGATTTATGCTGATGTTTAAAGAAATAGTGTGCAAAATCTACA 2098
QY 1440 ATATTTCTATGAAACATCCACAGGAAATGAAGCATACAGTTATCATTTGATTCCTT 1499
DB 2099 ATATTTCTATGAAACATCCACAGGAAATGAAGCATACAGTTATCATTTGATTCCTT 2158
QY 1500 TTTCTGCACTAAAAATTTTACAGAAATGCTTCCAAAGTTCAGCGAGACTCCAGAGACT 1559
DB 2159 TTTCTGCACTAAAAATTTTACAGAAATGCTTCCAAAGTTCAGCGAGACTCCAGAGACT 2218
QY 1560 TTGACAAAAGCAACCAATATGTTAAGATGATGATGATCACTCATGTTTCTGGAAT 1619
DB 2219 TTGACAAAAGCAACCAATATGTTAAGATGATGATGATCACTCATGTTTCTGGAAT 2278
QY 1620 GAGCATTTATGATCATTAAGGTTTACAGACAGAGCTTTTATAGGCAATGATCATATAG 1679
DB 2279 GAGCATTTATGATCATTAAGGTTTACAGACAGAGCTTTTATAGGCAATGATCATATAG 2338
QY 1680 CTCGAAGCAGCAACAAGATGAGAGGAGTCTATCCAGGAATTTTATGATGCTCTGT 1739
DB 2339 CTCGAAGCAGCAACAAGATGAGAGGAGTCTATCCAGGAATTTTATGATGCTCTGT 2398
QY 1740 TTGATATTTAAAGCAAAAGTGGACCTTCCAAAGGCTTGGGGAATGGAAGACAGATTT 1799
DB 2399 TTGATATTTAAAGCAAAAGTGGACCTTCCAAAGGCTTGGGGAATGGAAGACAGATTT 2458

OY 1800 CTGTTGACGCTTACAGTGCAGGACGCTGCAGACGCTTGAAGTGAAGTACCTTAAGAG 1859
| | | | |
DB 2459 ATGTTGACGCTTACAGTGCAGGACGCTGCAGACGCTTGAAGTGAAGTACCTTAAGAG 2518
| | | | |
OY 1860 ATCTTTAGAGACTCTGTAATGTAATTTGCTGTAAGTACCTC - AAAGAAATATATAG 1917
| | | | |
DB 2519 ATCTTTAGAGACTCTGTAATGTAATTTGCTGTAAGTACCTCAGAAAGATGCTAATG 2578
| | | | |
OY 1918 GATATTTGATTAATTTTAAATTTGTAATTTGTAATTAAGTGAATATATATATATAT 1977
| | | | |
DB 2579 GTATATTTGATTAATTTTAAATTTGTAATTTGTAATTAAGTGAATATATATATAT 2638
| | | | |
OY 1978 AAAAAAAAAAAAAA 1992
| | | | |
DB 2639 AAAAAAAAAAAAAA 2653
| | | | |

RESULT 3
US-08-705-477E-1
; Sequence 1, Application US/08705477E
; Patent No. 6569432
; GENERAL INFORMATION:
; APPLICANT: Israeli, Ron S
; APPLICANT: Heston, Warren D.W.
; APPLICANT: Fair, William R.
; APPLICANT: Overfelli, Ouathek
; APPLICANT: Plato, John
; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 1769/41426-G
; CURRENT APPLICATION NUMBER: US/08/705,477E
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2653
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-705-477E-1

Query Match 85.5%; Score 1702.6; DB 4; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

OY 240 AGGTTAAATATGCCCAGCTGCGAGGGGCCAAAGAGTCATCTCTACTCAGACCTGCTG 299
| | | | |
DB 899 AGTTAAATATGCCCAGCTGCGAGGGGCCAAAGAGTCATCTCTACTCAGACCTGCTG 958
| | | | |
OY 300 ACTACTTTGCTCTGGGGTGAAGTCCTATCCAGACGTTGGAATCTTCTGAGGTGGT 359
| | | | |
DB 959 ACTACTTTGCTCTGGGGTGAAGTCCTATCCAGATGTTGGAATCTTCTGAGGTGGT 1018
| | | | |
OY 360 TCCAGCGTGAATATCTCTAATCTGAATGTTGAGAGACCTCTCAGACAGGTTACC 419
| | | | |
DB 1019 TCCAGCGTGAATATCTCTAATCTGAATGTTGAGAGACCTCTCAGACAGGTTACC 1078
| | | | |
OY 420 CAGCAAAATGAATACCTTATAGGATGATGAGATTTGAGAGCTGTGGTCTTCCAAATATTC 479
| | | | |
DB 1079 CAGCAAAATGAATACCTTATAGGATGATGAGATTTGAGAGCTGTGGTCTTCCAAATATTC 1138
| | | | |
OY 480 CTGTTTCATCCAGTTGGATACATATGATGCACAGAAAGCTCCTAGAAAAATTTGGGTGGCTAG 539
| | | | |
DB 1139 CTGTTTCATCCAGTTGGATACATATGATGCACAGAAAGCTCCTAGAAAAATTTGGGTGGCTAG 1198
| | | | |
OY 540 CACACACGATAGAGCTGAGAGAGAGTCTCAAAAGTGTCTACAAATTTGGAGCTGGCT 599
| | | | |
DB 1199 CACACACGATAGAGCTGAGAGAGAGTCTCAAAAGTGTCTACAAATTTGGAGCTGGCT 1258
| | | | |
OY 600 TTACTGAAACTTTTCTACACAAAAAGTCAAGATGACATCCACTCTACCAATGAATGA 659
| | | | |
DB 1259 TTACTGAAACTTTTCTACACAAAAAGTCAAGATGACATCCACTCTACCAATGAATGA 1318
| | | | |
OY 660 CGAGATTTAAATGTGATAGTACTCTCAGAGGAGCGATGGAACCAACAGATATGTCA 719
| | | | |

DB 1319 CAAGATTTTACATGTGATAGTACTCTCAGAGAGACAGTGGAAACAGACAGATATGTCA 1378
| | | | |
OY 720 TTCTGGAGAGTCAACCGGACTCTAGGCTGTTTGGTGTATGACCTCAGAGTGGAGCAG 779
| | | | |
DB 1379 TTCTGGAGAGTCAACCGGACTCTAGGCTGTTTGGTGTATGACCTCAGAGTGGAGCAG 1438
| | | | |
OY 780 CTGTTTCATGAAACGTGAGAGGCTTTGGAACACTGAAAAAGAAAGGTTGGAGACTTA 839
| | | | |
DB 1439 CTGTTTCATGAAACGTGAGAGGCTTTGGAACACTGAAAAAGAAAGGTTGGAGACTTA 1498
| | | | |
OY 840 GAAGAACAAATTTGTTTGGCAAGCTGGGATGACAGAAATTTGCTCTTGTCTACTAG 899
| | | | |
DB 1499 GAAGAACAAATTTGTTTGGCAAGCTGGGATGACAGAAATTTGCTCTTGTCTACTAG 1558
| | | | |
OY 900 AGTGGGACAGAGTAATTTCAAGCTCTTCAAGAGCTGGCGCTGGCTTATATATATGCTG 959
| | | | |
DB 1559 AGTGGGACAGAGTAATTTCAAGCTCTTCAAGAGCTGGCGCTGGCTTATATATATGCTG 1618
| | | | |
OY 960 ACTCATCTATAGAGGAACTACACCTGAGAGTTGATTTGACACACATGATGTACAGCT 1019
| | | | |
DB 1619 ACTCATCTATAGAGGAACTACACCTGAGAGTTGATTTGACACACATGATGTACAGCT 1678
| | | | |
OY 1020 TGGTATCAACCTTAACAAAAGAGCTGAAAAGCCCTGATGAAGCTTTGAAAGCAATCTC 1079
| | | | |
DB 1679 TGGTATCAACCTTAACAAAAGAGCTGAAAAGCCCTGATGAAGCTTTGAAAGCAATCTC 1738
| | | | |
OY 1080 TTTATGAAGTTGGACTTAACAAAAGCTCTTCCAGAGTTCACTGAGATCCAGAGATA 1139
| | | | |
DB 1739 TTTATGAAGTTGGACTTAACAAAAGCTCTTCCAGAGTTCACTGAGATCCAGAGATA 1798
| | | | |
OY 1140 GCAAAATGGATCGGAAATGATTTTGAAGGTTCTTCCAGAGCTTGAATGCTTCTCAG 1199
| | | | |
DB 1799 GCAAAATGGATCGGAAATGATTTTGAAGGTTCTTCCAGAGCTTGAATGCTTCTCAG 1858
| | | | |
OY 1200 GCAGAGCAGGTATACTTAAATTTGGGAAACAAACAAATTCAGGCTATCCACTGATC 1259
| | | | |
DB 1859 GCAGAGCAGGTATACTTAAATTTGGGAAACAAACAAATTCAGGCTATCCACTGATC 1918
| | | | |
OY 1260 ACAGTGTCTATGAACATATGAGTGTGGGAAAAGTTTATGATTCGAATGTTAAATATC 1319
| | | | |
DB 1919 ACAGTGTCTATGAACATATGAGTGTGGGAAAAGTTTATGATTCGAATGTTAAATATC 1978
| | | | |
OY 1320 ACCATCAGTGGGCCAGAGTTGAGAGAGAGTGGTGTGAGTACGCCAATTCATAGTGC 1379
| | | | |
DB 1979 ACCATCAGTGGGCCAGAGTTGAGAGAGAGTGGTGTGAGTACGCCAATTCATAGTGC 2038
| | | | |
OY 1380 TCCCTTTGATTTGAGATTAATGCTGATTTTAAAGAAATGATGCTGACAAAATCTACA 1439
| | | | |
DB 2039 TCCCTTTGATTTGAGATTAATGCTGATTTTAAAGAAATGATGCTGACAAAATCTACA 2098
| | | | |
OY 1440 ATATTTCTATGAACATCCACAGGAATGAGATACAGTTCATTCATTTGATTCACCTT 1499
| | | | |
DB 2099 ATATTTCTATGAACATCCACAGGAATGAGATACAGTTCATTCATTTGATTCACCTT 2158
| | | | |
OY 1500 TTTCTGACGTAATAAATTTTACAGAAATTTGTTCCAAAGTTACAGGAGAGACTCCAGACT 1559
| | | | |
DB 2159 TTTCTGACGTAATAAATTTTACAGAAATTTGTTCCAAAGTTACAGGAGAGACTCCAGACT 2218
| | | | |
OY 1560 TTGACAAAAGCAACCAATATTTGTAAGATGATGATCAACTCATGTTTCTGGAAA 1619
| | | | |
DB 2219 TTGACAAAAGCAACCAATATTTGTAAGATGATGATCAACTCATGTTTCTGGAAA 2278
| | | | |
OY 1620 GAGCATTTATGATCATTAGAGTTTACAGACAGACCTTTTATATAGGATGATCTCATG 1679
| | | | |
DB 2279 GAGCATTTATGATCATTAGAGTTTACAGACAGACCTTTTATATAGGATGATCTCATG 2338
| | | | |
OY 1680 CTCGAAGCAGCACAACAAGTATGAGAGGAGTCAATTCAGAGATTTATGATGCTGCT 1739
| | | | |
DB 2339 CTCGAAGCAGCACAACAAGTATGAGAGGAGTCAATTCAGAGATTTATGATGCTGCT 2398
| | | | |
OY 1740 TTGATATTTGAAGCAAAAGTGAACCTTCCAAAGGCTGGGAGATGTAAGAGACAGATTT 1799
| | | | |
DB 2399 TTGATATTTGAAGCAAAAGTGAACCTTCCAAAGGCTGGGAGATGTAAGAGACAGATTT 2458
| | | | |

Db	2133	TTGATATTGGAAGCAACTGGACCTTCCAAAGCCCTGGGGAGAGTGAAGAGACAGATT	2192
Qy	1800	CTGTTCAGACCTTACAGTGCAGCAGCTGCAGAGACTTTAGTGAAGTACCCTAAGAGG	18559
Db	2193	ATGTTTGACGCTTACAGTGCAGCAGCTGCAGAGACTTTGAGTGAAGTACCCTAAGAGG	2252
Qy	1860	ATTCTTTAGAGACTCTGTATGAAATTGTGTATGTACTC--AAAGATTAATTAATGG	19177
Db	2253	ATTCTTTAGAGAAATCCGATTGAAATTGTGTGTATGTACTCAGAAAAGATTCGTAATGG	2312
Qy	1918	GTATATTTGATTAATTTTAAAAATTTGTATTTTGAATTAAGTTGAATTTATATATAAA	19777
Db	2313	GTATATTTGATTAATTTTAAAAATTTGTATTTTGAATTAAGTTGAATTTATATATAAA	2372
Qy	1978	AAAAAAAAAAAAAAAA 1992	
Db	2373	AAAAAAAAAAAAAAAA 2387	
RESULT 5			
US-09-164-034B-1			
GENERAL INFORMATION:			
APPLICANT: Moncheff, Milcho S.			
Loukinov, I. Dmitri			
Zoubek, Serguei			
TITLE OF INVENTION: Immunotherapy of Cancer Through Expression			
of Truncated Tumor- or Tumor-Associated Antigen			
NUMBER OF SEQUENCES: 1			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: William S. Ramsey,			
Ramsey, Cook, Looper & Kurlander, LLC			
STREET: 10420 Little Patuxent Parkway, Suite 250			
CITY: Columbia			
STATE: Maryland			
COUNTRY: USA			
ZIP: 21044			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage			
COMPUTER: PC			
OPERATING SYSTEM: Windows 95			
SOFTWARE: Wordperfect 8			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/164,034B			
FILING DATE: 30-Sep-1998			
ATTORNEY/AGENT INFORMATION:			
NAME: Ramsey, William S.			
REGISTRATION NUMBER: 32,715			
REFERENCE/DOCKET NUMBER: br11			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (410) 992-9660			
TELEFAX: (410) 992-9540			
SEQUENCE DESCRIPTION: SEQ ID NO: 1			
US-09-164-034B-1			
Query Match			
Best Local Similarity 79.3%; Score 1579.4; DB 4; Length 2133;			
Matches 1592; Conservative 0; Mismatches 21; Indels 0; Gaps 0;			
Qy	240	AGGTTAAAGAGCCAGCTGCAGGGGCGCAAGGAGTATCTCTACACAGCCCTGCTG	299
Db	512	AGGTTAAAGAGCCAGCTGCAGGGGCGCAAGGAGTATCTCTACACAGCCCTGCTG	571
Qy	300	ACTACTTGTGCTCGGGGGTGAAGTCTCATCCAGAGCGTTGGAAATCTCTGGAGGTGGT	359
Db	572	ACTACTTGTGCTCGGGGGTGAAGTCTCATCCAGAGCGTTGGAAATCTCTGGAGGTGGT	631
Qy	360	TCCAGCGTGAATAATCTCTAAATCTGAATGTGTGACAGAGACCTCTCACACAGGTATAC	419
Db	632	TCCAGCGTGAATAATCTCTAAATCTGAATGTGTGACAGAGACCTCTCACACAGGTATAC	691
Qy	420	CAGCAAAATGAATAGCTTATAGCGATGGAATTTGACAGAGCGTGTGGTCTTCCAAATATTC	479
Db	692	CAGCAAAATGAATAGCTTATAGCGCGTGAATTTGACAGAGCGTGTGGTCTTCCAAATATTC	751

QY	480	CTGTTCATCCAGTTGGTACTATGATGCACAGAAAGCTCCAGAAAAAATGGGTGCACG	539
Db	752	CTGTTCATCCAAATTGGATCTAGTACTAGTATGCACAGAAAGCTCTTAGAAAAAATGGGTGCACG	811
QY	540	CACCACCAGATAGCAGCTGGAGAGAGAGAGTCTCAAAGTGTCCTACAAATGTTGGACCTGGCT	599
Db	812	CACCACCAGATAGCAGCTGGAGAGAGAGTCTCAAAGTGTCCTACAAATGTTGGACCTGGCT	871
QY	600	TTTACTGGAACCTTTCTTACACAAAAAATCCAAGATGCACATCCACTCTACCAATGTAACGTA	659
Db	872	TTTACTGGAACCTTTCTTACACAAAAAATCCAAGATGCACATCCACTCTACCAATGTAACGTA	931
QY	660	CGAAGATTTCAATGTATAGTACTCTCAGAGAGACGATGGAACCGACAGATATGTCA	719
Db	932	CAGAAGATTTCAATGTATAGTACTCTCAGAGAGACGATGGAACCGACAGATATGTCA	991
QY	720	TTCTGGAGGTCACCGGGACTCATGGGTGTTGGTGATATTGACCTTCAGAGTGGACGAC	779
Db	992	TTCTGGAGGTCACCGGGACTCATGGGTGTTGGTGATATTGACCTTCAGAGTGGACGAC	1051
QY	780	CTGTGTTTCATGGAACCTGTGAGAGCTTTGGAACTGGAAGAAAAAGAGGGGTGGAGACCTA	839
Db	1052	CTGTGTTTCATGGAACCTGTGAGAGCTTTGGAACTGGAAGAAAAAGAGGGGTGGAGACCTA	1111
QY	840	GAAAGAACAAATTTGTTTGGCAAGCGGGGATGCAGAGAAATTTGTCCTCTTGGTTCCTACTG	899
Db	1112	GAAAGAACAAATTTGTTTGGCAAGCGGGGATGCAGAGAAATTTGTCCTCTTGGTTCCTACTG	1171
QY	900	AGTGGGACAGAGATAAATTCAAGACTCCTTCAGAGCGTGCGGTGGCTTATATTATGCTG	959
Db	1172	AGTGGGACAGAGATAAATTCAAGACTCCTTCAGAGCGTGCGGTGGCTTATATTATGCTG	1231
QY	960	ACATCATCTATAGAGGAACACTACACTCGTAGAGTTGATTGTACACACTGATGTACAGCT	1019
Db	1232	ACATCATCTATAGAGGAACACTACACTCGTAGAGTTGATTGTACACACTGATGTACAGCT	1291
QY	1020	TGGATTTCACAACCTTAACAAAAGAGCTGTAAAGCCCTGATGGAAGGCTTTGAAGGCAAACTC	1079
Db	1292	TGGATTTCACAACCTTAACAAAAGAGCTGTAAAGCCCTGATGGAAGGCTTTGAAGGCAAACTC	1351
QY	1080	TTTATGAAAGTTGGACTTAATAAAAAAGTCCTTCCACAGACTCAGTGGCATGCCCCAGGATA	1139
Db	1352	TTTATGAAAGTTGGACTTAATAAAAAAGTCCTTCCACAGACTCAGTGGCATGCCCCAGGATA	1411
QY	1140	GCAAAATGGGATCGGAAATGATTTTGAAGGTCTTCCAAACGACTTGGAAATGCTCTCAG	1199
Db	1412	GCAAAATGGGATCGGAAATGATTTTGAAGGTCTTCCAAACGACTTGGAAATGCTCTCAG	1471
QY	1200	GCAAGACGAGGTATACTAAAAAATTTGGGAAACAAAAATTCAGGCGGCTATCCACTGTATC	1259
Db	1472	GCAAGACGAGGTATACTAAAAAATTTGGGAAACAAAAATTCAGGCGGCTATCCACTGTATC	1531
QY	1260	ACAGTGTCTATGAACAATATGAGATTTGGTGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1319
Db	1532	ACAGTGTCTATGAACAATATGAGATTTGGTGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1591
QY	1320	ACGTCACATGNGGCCAGGTTGAGAGAGGAGATGATTTGAGCTGAGCCAAATTCACATAGTC	1379
Db	1592	ACGTCACATGNGGCCAGGTTGAGAGAGGAGATGATTTGAGCTGAGCCAAATTCACATAGTC	1651
QY	1380	TCCCTTTTGAATGTGAGATTAATGCTGTAGTTTAAAGAAATATGCTGACAAAAATCTACA	1439
Db	1652	TCCCTTTTGAATGTGAGATTAATGCTGTAGTTTAAAGAAATATGCTGACAAAAATCTACA	1711
QY	1440	ATATTTCTATGAAACATCCACAGAAATGAAGACATACAGTTTATCATTTTATTCACATTT	1499
Db	1712	ATATTTCTATGAAACATCCACAGAAATGAAGACATACAGTTTATCATTTTATTCACATTT	1771
QY	1500	TTTCTGAGTAAAAAATTTTACAGAAATTTGCTTCCAGATTTAGGAGAGAGACTCCAGAGACT	1559
Db	1772	TTTCTGAGTAAAAAATTTTACAGAAATTTGCTTCCAGATTTAGGAGAGAGACTCCAGAGACT	1831

SEQUENCE CHARACTERISTICS:
LENGTH: 893 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-45

Query Match 11.2%; Score 223.2; DB 2; Length 893;
Best Local Similarity 92.8%; Pred. No. 8.6e-50;
Matches 256; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

QY 1 AGCAATACCTACCTACCAATTAAGAAATTCACAAATCTGATGTTCTGAGATTTTGA 60
DB 275 AGCAATACCTACCTACCAATTAAGAAATTCACAAATCTGATGTTCTGAGATTTTGA 216
QY 61 GAGCTTATAGTACGAAAGAAAGGAAATTCCTCTGAGATGCTCTTTTGTAGGCC 120
DB 215 CAGCTTATAGTACGAAAGAAAGGAAATTCCTCTGAGATGCTCTTTTGTAGGCC 157
QY 121 TAAAGA-CAAAAGTTGAGTAAGTAAGTTCTATCTATTAAGTGAATTAATTT 179
DB 156 TAAAGAGAAAGAGTTGAGTAAGTAAGTTCTATCTATTAAGTGAATTAATTT 97
QY 180 GATATTAACAATCTGACAAACCAATTTAAATTAAGAAAGAAAGACACTGTCTTCT 239
DB 96 GATATTAACAATCTGACAAACCAATTTAAATTAAGAAAGAAAGACACTGTCTTCT 37
QY 240 AGGTTAAATGCCCCAGCTGCGAGGCGCAAGAG 275
DB 36 AGGTTAAATGCCCCAGCTGCGAGGCGCAAGAG 1

RESULT 9
US-09-439-313-454/c
Sequence 454, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 454
LENGTH: 231
TYPE: DNA
ORGANISM: Homo sapiens
US-09-439-313-454

Query Match 11.1%; Score 220.2; DB 4; Length 231;
Best Local Similarity 98.7%; Pred. No. 2.9e-49;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 778 AGCTGTTGTCATGAAACCTGTGAGAGCTTTGGACACGAAAGAGGTTGAGACC 837
DB 231 AGCTGTTGTCATGAAACCTGTGAGAGCTTTGGACACGAAAGAGGTTGAGACC 172
QY 838 TAGAAGACAATTTTGTTCAGAGCTGAGATGCAAGAAATTTGCTCTTGTCTAC 897
DB 171 TAGAAGACAATTTTGTTCAGAGCTGAGATGCAAGAAATTTGCTCTTGTCTAC 112
QY 898 TGAGTGGCAGAGATTAATTCAGACTCTTCAAGACCGTGGCGCTTATTTAATGC 957
DB 111 TGAGTGGCAGAGATTAATTCAGACTCTTCAAGACCGTGGCGCTTATTTAATGC 52
QY 958 TGACTCATCTATAGAGAACTACACTCTGAGAGTTGATTGTAC 1002
DB 51 TGACTCATCTATAGAGAACTACACTCTGAGAGTTGATTGTAC 7

RESULT 10
US-09-352-616A-454/c
Sequence 454, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 454
LENGTH: 231
TYPE: DNA
ORGANISM: Homo sapiens
US-09-352-616A-454

Query Match 11.1%; Score 220.2; DB 4; Length 231;
Best Local Similarity 98.7%; Pred. No. 2.9e-49;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 778 AGCTGTTGTCATGAAACCTGTGAGAGCTTTGGACACGAAAGAGGTTGAGACC 837
DB 231 AGCTGTTGTCATGAAACCTGTGAGAGCTTTGGACACGAAAGAGGTTGAGACC 172
QY 838 TAGAAGACAATTTTGTTCAGAGCTGAGATGCAAGAAATTTGCTCTTGTCTAC 897
DB 171 TAGAAGACAATTTTGTTCAGAGCTGAGATGCAAGAAATTTGCTCTTGTCTAC 112
QY 898 TGAGTGGCAGAGATTAATTCAGACTCTTCAAGACCGTGGCGCTTATTTAATGC 957
DB 111 TGAGTGGCAGAGATTAATTCAGACTCTTCAAGACCGTGGCGCTTATTTAATGC 52
QY 958 TGACTCATCTATAGAGAACTACACTCTGAGAGTTGATTGTAC 1002
DB 51 TGACTCATCTATAGAGAACTACACTCTGAGAGTTGATTGTAC 7

RESULT 11
US-08-325-553-27
Sequence 27, Application US/0832553
Patent No. 5538866
GENERAL INFORMATION:
APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2003, 19:30:56 : Search time 649 Seconds
(without alignments)
7829.460 Million cell updates/sec

Title: US-09-973-382c-1
Perfect score: 1992
Sequence: 1 agcaatactcactaccacac.....taaaaaaaaaaaaaaaaa 1992

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues
Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1702.6	85.5	2653	10	US-09-969-708-536	Sequence 536, App
2	1702.6	85.5	2653	12	US-09-873-319-451	Sequence 451, App
3	1702.6	85.5	2653	12	US-09-960-706-716	Sequence 716, App
4	1702.6	85.5	2653	12	US-10-210-120-5	Sequence 5, Appli
5	1702.6	85.5	2653	14	US-10-094-699-2	Sequence 2, Appli
6	1702.6	85.5	2653	14	US-10-205-823-111	Sequence 131, App
7	1687.2	84.7	2558	10	US-09-978-295A-617	Sequence 617, App
8	1687.2	84.7	2558	10	US-09-978-697-617	Sequence 617, App
9	1687.2	84.7	2558	10	US-09-978-192A-617	Sequence 617, App
10	1687.2	84.7	2558	10	US-09-999-832A-617	Sequence 617, App
11	1687.2	84.7	2558	11	US-09-978-189-617	Sequence 617, App
12	1687.2	84.7	2558	11	US-09-978-608A-617	Sequence 617, App
13	1687.2	84.7	2558	11	US-09-978-585A-617	Sequence 617, App
14	1687.2	84.7	2558	11	US-09-978-191A-617	Sequence 617, App
15	1687.2	84.7	2558	11	US-09-978-403A-617	Sequence 617, App
16	1687.2	84.7	2558	11	US-09-978-564A-617	Sequence 617, App

17	1687.2	84.7	2558	11	US-09-999-833A-617	Sequence 617, App
18	1687.2	84.7	2558	11	US-09-981-915A-617	Sequence 617, App
19	1687.2	84.7	2558	11	US-09-978-824-617	Sequence 617, App
20	1687.2	84.7	2558	11	US-09-918-585A-617	Sequence 617, App
21	1687.2	84.7	2558	11	US-09-978-423A-617	Sequence 617, App
22	1687.2	84.7	2558	11	US-09-978-193A-617	Sequence 617, App
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27	1687.2	84.7	2558	12	US-09-978-188A-617	Sequence 617, App
28	1687.2	84.7	2558	12	US-09-978-298A-617	Sequence 617, App
29	1687.2	84.7	2558	12	US-10-143-031A-617	Sequence 617, App
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31	1687.2	84.7	2558	12	US-10-017-083A-617	Sequence 617, App
32	1687.2	84.7	2558	12	US-10-143-030A-617	Sequence 617, App
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34	1687.2	84.7	2558	12	US-10-187-749-103	Sequence 103, App
35	1687.2	84.7	2558	12	US-10-194-457-103	Sequence 103, App
36	1687.2	84.7	2558	12	US-10-145-128A-617	Sequence 617, App
37	1687.2	84.7	2558	12	US-10-186-642-103	Sequence 103, App
38	1687.2	84.7	2558	12	US-10-196-747-103	Sequence 103, App
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43	1687.2	84.7	2558	12	US-10-173-694-103	Sequence 103, App
44	1687.2	84.7	2558	12	US-10-173-695-103	Sequence 103, App
45	1687.2	84.7	2558	12	US-10-173-696-103	Sequence 103, App

ALIGNMENTS

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RESULT 1
US-09-969-708-536
; Sequence 536, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
; FILE REFERENCE: 689290-70
; CURRENT APPLICATION NUMBER: US/09/969,708
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: US/60/237,606
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,608
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,425
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 536
; LENGTH: 2653
; TYPE: DNA
; ORGANISM: Homosapiens
US-09-969-708-536

Query Match      85.5%; Score 1702.6; DB 10; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

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QY 300 ACTACTTCTCTCTGGGGTGAATCTCTATTCACAGAGTCTTCTCTGGAGGTTG 359
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DB 959 ACTACTTCTCTCTGGGGTGAATCTCTATTCACAGAGTCTTCTCTGGAGGTTG 1018
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QY 360 TCCAGCGTGAATATCTGAATCTGAATGTGGTCAGAGACCCCTCTACACAGGTTACC 419
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D	b	1079	CACCAATATGAATATGCTTATATAGCGCTGGAAATTGCAGAGGCTGTGGTCTTCCAAAGTATTC	1138
O	y	480	CTGTGATCCAGTTGGATCTATATGATGTCACAGAAAGCTCCATAGAAAAATGGGAGGCTCAG	539
D	b	1139	CTGTTCATCCAAATGGATCTATATGATGTCACAGAAAGCTCCATAGAAAAATGGGAGGCTCAG	1198
O	y	540	CACCACCAAGATAGACGCTGAGAGAGGAAGTCTCAAAGTGTCTCAAAATGTTGGAACCTGGCT	599
D	b	1199	CACACCAAGATAGAGCTGGAGAGGAAGTCTCAAAAGTGGCCCTCAAAATGTTGGAACCTGGCT	1258
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O	y	660	CGAATTTCAATGATATAGTATAGTATCTCAGAGAGCAGTGGGAACCGACAGATATGTCA	719
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D	b	1379	TTCTGAGAGTTCACCCGGAGCTCATGGGTGTGGTGGTATATGACCTCCAGAGTGGACAG	1438
O	y	780	CTGTGTTTCATGAATCTGTGAGAGCTTTGGAACATCGAAAAAGGAAGGCTGAGACCTTA	839
D	b	1439	CTGTGTTTCATGAATCTGTGAGAGCTTTGGAACATCGAAAAAGGAAGGCTGAGACCTTA	1498
O	y	840	GAAACAACAATTTTGTTCGAAGCTGGGATGTCAGAAATTTGGTCTCTTGGTCTTACTG	899
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D	b	1559	AGTGGGCGAGAGTAAATTCGAAGTCTCTCAGAAGCTGGCGTGGCTTATATTAATCTG	1618
O	y	960	ACTCATCTATATGAAGGAAATCTACACTCTGAGAGTTGATTGTACACCACTGATGTACAGT	1019
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O	y	1320	ACCTACACTGTGGCCAGGTTTCGAGAGAGGATGTGTGTTGACCTAGCCAAATTCATATAGTC	1379
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O	y	1440	ATATTTCTATGAACATCTCAGAGGAATGAAGACATACAGTTTATCATTTGATTCACCTT	1499
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Db	2339	CTCCAGACAGCCCAACAAAGTATTCAGGAGGAGTATTCACAGAAATTTATGATCTCTGT	2398
QY	1740	TTGATATTGGAAGCAAGTGGACCTTCACAGGCTGGGAGAGTGCAGAGACAGATTT	1799
Db	2399	TTGATATTGGAAGCAAGTGGACCTTCACAGGCTGGGAGAGTGCAGAGACAGATTT	2458
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QY	1860	ATTCTTTAGAGACTCTGTATTGAATTTGTGTGTATGTCACTC--AAAGATTAATAATG	1917
Db	2519	ATTCTTTAGAGAAATCCGATTAATGTAATTTGTGTGTATGTCACTCAGAAAGATCCGTAATG	2578
QY	1918	GTAATATTGATTAATTTTAAAAATTTGGTATATTGGAATTAAGTGAATATTTAATATAAA	1977
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Db	2639	AAAAAAAAAAAAAAAAA 2653	

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RESULT 2
US-09-873-319-451
Sequence 451, Application US/09873319A
Publication No. US20030134324A1
GENERAL INFORMATION:
APPLICANT: Munger, William E.
APPLICANT: Kulkarni, Prakash
APPLICANT: Getzenberg, Robert H.
APPLICANT: Waga, Iwao
APPLICANT: Yamamoto, Jun
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic
TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles
FILE REFERENCE: 44921-5029-US
CURRENT APPLICATION NUMBER: US/09/873, 319A
CURRENT FILING DATE: 2001-06-05
EARLIER APPLICATION NUMBER: US 60/223,323
EARLIER FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 451
LENGTH: 2653
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20030134324A1 M99487
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Db	899	AGGTTAAAAATGCCAGCTGGCAGGAGGCGCAAGAGAGTCATCTCTACTACGACCTGCTG	958						

OY	240	AGGTTAAATATGCCACCTGGCAGGGGCGCAAAGAGCATCTTCTACTCGACCCCTCTG	299
Db	899	AGGTTAAATATGCCACCTGGCAGGGGCGCAAAGAGCATCTTCTACTCGACCCCTCTG	958
OY	300	ACTACTTTGCTCCTGGGGTGAAGTCTATCCAGACGGTTGGAAATCTTCTGAGAGTGCTG	359
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OY	420	CAGCAATATGATACGCTTATATAGGCATGGAATTGGACAGGGCTGTGTGCTTCCAAATATTC	479
Db	1079	CAGCAATATGATATATGCTTATATAGGCATGGAATTGGACAGGGCTGTGTGCTTCCAAATATTC	1138
OY	480	CTGTTCATCCAGTTGGATCTATGATATCACAGAAAGCTCTTGAAGAAAAATGGTGGCTCAG	539
Db	1139	CTGTTCATCCAAATTTGGATCTATGATATCACAGAAAGCTCTTGAAGAAAAATGGTGGCTCAG	1198
OY	540	CACCAACCAATAGCAGCTGGAGAGAGAGTCCAAAGTGTCTTACAAATTTGGACCTGGCT	599
Db	1199	CACCAACCAATAGCAGCTGGAGAGAGAGTCCAAAGTGTCTTACAAATTTGGACCTGGCT	1258
OY	600	TTACTGGAAACCTTTCTTACACAAAAAGTCAAGATGCACATCCACTCTTACCAATGAATGA	659
Db	1259	TTACTGGAAACCTTTCTTACACAAAAAGTCAAGATGCACATCCACTCTTACCAATGAATGA	1318
OY	660	CGACAATTTTCAATGCTATGCTGTCTCCAGAGAGAGAGTGGAAACGACACAGATATATGCA	719
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OY	720	TTCTGGGAGGTCACCGGGACTCATGGGTGTGTTGGTGTATTTGACCCCTCAGAGTGGACAG	779
Db	1379	TTCTGGGAGGTCACCGGGACTCATGGGTGTGTTGGTGTATTTGACCCCTCAGAGTGGACAG	1438
OY	780	CTGTGTTTTCATGAAGACGTGAGAGCTTTGGAAACACTGAAAAAGGAGGGTGGAGACTTA	839
Db	1439	CTGTGTTTTCATGAAGAAATGTGAGAGCTTTGGAAACACTGAAAAAGGAGGGTGGAGACTTA	1498
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OY	900	AGTGGGCAAGAGATTAATTCAGACTCCTTCAGAGCCTGGCTGGCTTATATTAATGCTG	959
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Db	1679	TGCTATACAAACCTTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGCAAAATCTC	1738
OY	1080	TTTATATGAAGTTGGACATTAAGAAAGCTCTTCCACAGATTTAGTGGCATGCCCCAGATATA	1139
Db	1739	TTTATATGAAGTTGGACATTAAGAAAGCTCTTCCACAGATTTAGTGGCATGCCCCAGATATA	1798
OY	1140	GCAAAATTTGGAGTCTGGAATATGTTTGGAGTGTCTTCCAAACGACTTGGAAATTCCTTCAG	1199
Db	1799	GCAAAATTTGGAGTCTGGAATATGTTTGGAGTGTCTTCCAAACGACTTGGAAATTCCTTCAG	1858
OY	1200	GCAGAGCAGGATATCTAATAAATTGGGAACAAACAAATTTAGCGGCTATCCACTGATATC	1259
Db	1859	GCAGAGCAGGATATCTAATAAATTGGGAACAAACAAATTTAGCGGCTATCCACTGATATC	1918
OY	1260	ACAGTGTCTATGAAGACATATGATTTGGGAGAAAGTTTATGATCCAAATGTTTAAATATTC	1319
Db	1919	ACAAGTGTCTATGAAGACATATGATTTGGGAGAAAGTTTATGATCCAAATGTTTAAATATTC	1978
OY	1320	ACCTCCTACTGTGGCCAGGTTCCAGAGAGGAGTGTGTTGACTATGACCAATTCACATATGATGC	1379

Db	1979	ACCTCACTGTGGCCACAGGTTGAGAGAGGAAATGGTTTGGAGCTAGGCCAATTCCTATGTGC	2038
QY	1380	TCCTTTTGATTTGTCCGAGATTATGCTGTACTTTTAAAGATATGCGACAAATCTACAA	1439
Db	2039	TCCCTTTTGATTTGTGCGAGATTATGCTGTAGTTTAAAGATATGCTGACAAATCTTACA	2098
QY	1440	ATATTTCTATGAACAATCACTCACAGGAATGAAGACATACAGTTATATCAATTGATTCACATT	1499
Db	2099	GTAATTTCTATGAACAATCACTCACAGGAATGAAGACATACAGTGTATCAATTTGATTCACATT	2158
QY	1500	TTTCTGCGATGAAAAATTTTACAGAAATTCCTTCCAAAGTTTCAGGCAAGACCTCAGAGACT	1559
Db	2159	TTTCTGCGATGAAAAATTTTACAGAAATTCCTTCCAAAGTTTCAGGCAAGACCTCAGAGACT	2218
QY	1560	TTGCAAAACCAACCCCAATTTGTTAAGATGATGATGATCACTCATGTCTTCTGGAAA	1619
Db	2219	TTGCAAAACCAACCCCAATTTTATTAAGATGATGATGATCACTCATGTCTTCTGGAAA	2278
QY	1620	GAGCATTTATTTGATTCATTTAGGGTTTACACAGACAGACCTTTTATAGGCATGTCAATATG	1679
Db	2279	GAGCATTTATTTGATTCATTTAGGGTTTACACAGACAGACCTTTTATAGGCATGTCAATATG	2338
QY	1680	CTCCACACAGCCACACAAAGATATTCACAGGAGAGTATCCACAGAAATTTATAGTCTCTGT	1739
Db	2339	CTCCACACAGCCACACAAAGATATTCACAGGAGAGTATCCACAGAAATTTATGATCTCTGT	2398
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Db	2399	TTGATATTGGAAGCAAGAGTGGACCTTCCAAAGGCTTGCGGAGAGTGAAGACAGATT	2458
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Db	2459	ATGTTTCAGACCTTGACAGTGCAGGACAGCTGCAGAGACTTTGATGAGTAAGTACCTTAAGAG	2518
QY	1860	ATTTCTTAGAGACTCTGTATGAAATTTGTGTGATGTCACTC--AAAGATATATTAATGG	1917
Db	2519	ATTTCTTAGAGAAATCCGTATGATTTGTGTGATGTCACTCAGAAAGATTCGTAAATGG	2578
QY	1918	GTAATATTGATTAATTTTAAAAATTCGTATTTTGAAGATTAAGTGAATATTATATATAAAA	1977
Db	2579	GTAATATTGATTAATTTTAAAAATTCGTATTTTGAAGATTAAGTGAATATTATATATAAAA	2638
QY	1978	AAAAAAAAAAAAAAAA 1992	
Db	2639	AAAAAAAAAAAAAAAA 2653	
RESULT 4			
US-10-210-120-5			
Sequence 5, Application US/10210120			
Publication No. US20030175736A1			
GENERAL INFORMATION:			
APPLICANT: Chinaiyalan, Arul M.			
APPLICANT: Rudin, Mark A.			
APPLICANT: Sreekumar, Arun			
TITLE OF INVENTION: Expression Profile of Prostate Cancer			
FILE REFERENCE: IM-07221			
CURRENT APPLICATION NUMBER: US/10/210,120			
CURRENT FILING DATE: 2002-08-01			
PRIOR APPLICATION NUMBER: US 60/309,581			
PRIOR FILING DATE: 2001-08-02			
PRIOR APPLICATION NUMBER: US 60/334,468			
PRIOR FILING DATE: 2001-11-15			
NUMBER OF SEQ ID NOS: 123			
SOFTWARE: Patentin version 3.2			
SEQ ID NO 5			
LENGTH: 2653			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-10-210-120-5			
Query Match			
85.5%, Score 1702.6; DB 12; Length 2653;			

Query Match	85.5%	Score 1702.6	DB 14	Length 2653	
Best Local Similarity	98.5%	Pred. No. 0			
Matches 1729	Conservative	0	Mismatches	24	Indels 2; Gaps 1;
OY	240	AGGTTAAATGCGCCAGCTGGCAGGGGGCCAAAGAGTCAATTCTACTAGACCCGCTG	299		
Db	899	AGGTTAAAAATGCGCCAGCTGGCAGGGGGCCAAAGAGTCAATTCTACTCGACCCGCTG	958		
OY	300	ACTACTTTGCTCCTCGGGGTGAAGTCTTCCAGACGGTTGGAAVCTTCTCGAGGTGTC	359		
Db	959	ACTACTTTGCTCCTCGGGGTGAAGTCTTCCATCCAGATGTTGGAAVCTTCTCGAGGTGTC	1018		
OY	360	TCCAGCGTGGAAATATCTTAAATCTGAATGTGCAGAGAACCCCTCCACACCGAGTTAC	419		
Db	1019	TCCAGCGTGGAAATATCTTAAATCTGAATGTGCAGAGAACCCCTCCACACCGAGTTAC	1078		
OY	420	CAGCAATGAAATACGGTTATAGCATAGAAATTGCAGAGGCTGTGGTCTTCCAAAGTATTC	479		
Db	1079	CAGCAATGAAATATGCTTATAGCGCTGGAATTCAGAGGCTGTGGTCTTCCAAAGTATTC	1138		
OY	480	CTGTTCATCCAGTTGGATGACTATGATGCACAGAGCTCCTAGAAAAAATGGGTGGCTCAG	539		
Db	1139	CTGTTCATCCAAATTGGATGACTATGATGCACAGAGCTCCTAGAAAAAATGGGTGGCTCAG	1198		
OY	540	CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCTTCAAAATGTTGAGACCTGGCT	599		
Db	1199	CACCACCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGTCTTCAAAATGTTGAGACCTGGCT	1258		
OY	600	TTTACTGGAACCTTTCTTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA	659		
Db	1259	TTTACTGGAACCTTTCTTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA	1318		
OY	660	CGAAGATTTACAAATGTGATAGTACTCTCAGAGAGCAGTGGAAACAGACAGATATGTCA	719		
Db	1319	CAAGAATTTACAAATGTGATAGTACTCTCAGAGAGCAGTGGAAACAGACAGATATGTCA	1378		
OY	720	TTCCTGGAGGCTACCCGGGACTCAATGGGTGTTGGTGTATTGGTACCCCTCAGAGTGGACAG	779		
Db	1379	TTCCTGGAGGCTACCCGGGACTCAATGGGTGTTGGTGTATTGGTACCCCTCAGAGTGGACAG	1438		
OY	780	CTGTGTTTCATGAAACCTGTGAGAGCTTTTGGAACTGAAAAAGAGAGGTGAGACCTA	839		
Db	1439	CTGTGTTTCATGAAATGTGTAGAGGCTTTTGGAACTGAAAAAGAGAGGTGAGACCTA	1498		
OY	840	GAAGAACAATTTGTTTGCAGAGCTGGAGTGCAGAAATTTGCTTCTTGCTTCTACTG	899		
Db	1499	GAAGAACAATTTGTTTGCAGAGCTGGAGTGCAGAAATTTGCTTCTTGCTTCTACTG	1558		
OY	900	AGTGGGCGAGAGATTAATTCAGAGCTCCTTCAAGAGCGTGGGTGGCTTATTTAATCCTG	959		
Db	1559	AGTGGGCGAGAGATTAATTCAGAGCTCCTTCAAGAGCGTGGGTGGCTTATTTAATCCTG	1618		
OY	960	ACTCATCTATGGAAGAAATACACACTGTGAGATGTGAATTGACACCACTGATGTACAGCT	1019		
Db	1619	ACTCATCTATGGAAGAAATACACACTGTGAGATGTGAATTGACACCGTATGTACAGCT	1678		
OY	1020	TGCTATACAACTTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAAGCAATCTC	1079		
Db	1679	TGCTATACAACTTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAAGCAATCTC	1738		
OY	1080	TTTATGAAAGTTGGACATTAATAAAGTCTTCCCAAGATTAAGTGGCATGCCAGAGATAA	1139		
Db	1739	TTTATGAAAGTTGGACATTAATAAAGTCTTCCCAAGATTAAGTGGCATGCCAGAGATAA	1798		
OY	1140	GCAAATGGGAGCTCGGAAATGATTTTGGTGGTCTTCCCAACGACTTGGCATTCCTTCAG	1199		
Db	1799	GCAAATGGGAGCTCGGAAATGATTTTGGTGGTCTTCCCAACGACTTGGCATTCCTTCAG	1858		
OY	1200	GCAGAGCAGCGTATACTAAAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATC	1259		
Db	1859	GCAGAGCAGCGTATACTAAAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATC	1918		
OY	1260	ACAGGTCTATGAACAATAGATGTTGGTGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1319		

Db	1919	ACAGTGTCTATGAAACCTATGAGTGTGGTGAAGAAAGTTTATATGATCCAAATGTTTAAATATTC	1978
QY	1320	ACCTCACTGTGGCCCGCAGGTTCGAGAGAGGATGCTGTTTGACGTACGCCAATTCATATGTCG	1379
Db	1979	ACCTCACTGTGGCCCGCAGGTTCGAGAGAGGATGCTGTTTGACGTACGCCAATTCATATGTCG	2038
QY	1380	TCCCTTTTGAATGTGTCAGATTAATGCTGTACTTTTAAGAAAGTATGCTGCACAAATCTTACA	1439
Db	2039	TCCCTTTTGAATGTGTCAGATTAATGCTGTACTTTTAAGAAAGTATGCTGCACAAATCTTACA	2098
QY	1440	AATTTCTATGAAGAACATCCACAGAAATGAAGACATACATTAATCATTTGATTCACCTT	1499
Db	2099	GTATTTCTATGAAGAACATCCACAGAAATGAAGACATACATTAATCATTTGATTCACCTT	2158
QY	1500	TTTCTGCAGTAAAAAATTTTACAGAAATTCCTTCCAAAGTTCAAGCGAGACCTCCAGACT	1559
Db	2159	TTTCTGCAGTAAAAAATTTTACAGAAATTCCTTCCAAAGTTCAAGCGAGACCTCCAGACT	2218
QY	1360	TTGCAAAAGACACCCCAATATGTTAAGATGATGAATGATCAACATCATGTTCTGTGAAA	1619
Db	2219	TTGCAAAAGACACCCCAATATGTTAAGATGATGAATGATCAACATCATGTTCTGTGAAA	2278
QY	1620	GAGATTTATTTGATTCATTAAGGCTTACACAGACACCTTTTATAGCATGTCATCTATG	1679
Db	2279	GAGATTTATTTGATTCATTAAGGCTTACACAGACACCTTTTATAGCATGTCATCTATG	2338
QY	1680	CTCCACAGCAGCCACACACAGATATGACAGGGAGTCAATCCACAGAAATTTATGATGCTGTG	1739
Db	2339	CTCCACAGCAGCCACACACAGATATGACAGGGAGTCAATCCACAGAAATTTATGATGCTGTG	2398
QY	1740	TTGATATTTGAAGAAAGTGGACCCCTTCCAAAGCCTGGGAGATGTGAAGACAGATTT	1799
Db	2399	TTGATATTTGAAGAAAGTGGACCCCTTCCAAAGCCTGGGAGATGTGAAGACAGATTT	2458
QY	1800	CTGTATTCAGCCTTACACAGTGCAGCAGCTGCAGAGACCTTTAGTGAAGTACCTTAAGAG	1859
Db	2459	ATGTTTGCAGCCTTACACAGTGCAGCAGCTGCAGAGACCTTTAGTGAAGTACCTTAAGAG	2518
QY	1860	ATTCTTTAGACACTCTGTATTGAATTTGTGTGTAATCTC- --AAAGATAATTAATGC	1917
Db	2519	ATTCTTTAGACACTCTGTATTGAATTTGTGTGTAATCTC- --AAAGATAATTAATGC	2578
QY	1918	GTAATATGATATAATTTTAAATTTGCTATATTTTGAATAAAGTGAATATATATATATAA	1977
Db	2579	GTAATATGATATAATTTTAAATTTGCTATATTTTGAATAAAGTGAATATATATATATAA	2638
QY	1978	AAAAAAAAAAAAAAAA 1992	
Db	2639	AAAAAAAAAAAAAAAA 2653	
RESULT 6			
US-10-205-823-131			
Sequence 131, Application US/10205823			
Publication No. US20030108963A1			
GENERAL INFORMATION:			
APPLICANT: Schlegel, Robert			
APPLICANT: Monahan, John E.			
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APPLICANT: Gannavarapu, Manjula			
APPLICANT: Gordatcheva, Bella			
APPLICANT: Hoersch, Sebastian			
APPLICANT: Kamatkar, Shubhangi			
APPLICANT: Womsey, Angela M.			
APPLICANT: Glatt, Karen			
APPLICANT: Zhao, Xumei			
APPLICANT: Anderson, Dustin			
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND			
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND			
THERAPY OF PROSTATE CANCER			
FILE REFERENCE: MRI-044			
CURRENT APPLICATION NUMBER: US/10/205,823			

: CURRENT FILING DATE: 2002-07-25
: PRIOR APPLICATION NUMBER: 60/307,982
: PRIOR FILING DATE: 2001-07-25
: PRIOR APPLICATION NUMBER: 60/314,356
: PRIOR FILING DATE: 2001-08-22
: PRIOR APPLICATION NUMBER: 60/325,020
: PRIOR FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: 60/341,746
: PRIOR FILING DATE: 2001-12-12
: PRIOR APPLICATION NUMBER: 60/362,158
: PRIOR FILING DATE: 2002-03-05
: NUMBER OF SEQ ID NOS: 455
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 131
: LENGTH: 2653
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-205-823-131

Query Match 85.5%; Score 1702.6; DB 14; Length 2653;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1729; Conservative 0; Mismatches 24; Indels 2; Gaps 1;

QY 240 AGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGAGTCATTCTTACTCAGACCTGCTG 299
DB 899 AGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGAGTCATTCTTACTCAGACCTGCTG 958
QY 300 ACTACTTGTCTCTGGGGTGAAGTCCCTATCCACAGCGTTGGATCTTCTGGAGGTGTG 359
DB 959 ACTACTTGTCTCTGGGGTGAAGTCCCTATCCAGATGGTTGGAACTCTTCTGGAGGTGTG 1018
QY 360 TCCAGCGTGAATATCTCTAAATCTGAATGTCAGAGAGACCTCTCACACAGTTACC 419
DB 1019 TCCAGCGTGAATATCTCTAAATCTGAATGTCAGAGAGACCTCTCTCACACAGTTACC 1078
QY 420 CAGCAATGAAATACGCTTATAGGCAATGAAATTCAGAGGCTGTGGTCTTCCAAATATTC 479
DB 1079 CAGCAATGAAATACGCTTATAGGCGTGAATTCAGAGGCTGTGGTCTTCCAAATATTC 1138
QY 480 CTGTTCATCCAGTGTGATATCTATGATGCAAGAACTCCCTAGAAAAATGGGTGCTCAG 539
DB 1139 CTGTTCATCCAGTGTGATATCTATGATGCAAGAACTCCCTAGAAAAATGGGTGCTCAG 1198
QY 540 CACCACAGATAGCAGCTGGAGAGAACTCTCAAAGTGTCTCTCAATGTTGACCTGCT 599
DB 1199 CACCACAGATAGCAGCTGGAGAGAACTCTCAAAGTGTCTCTCAATGTTGACCTGCT 1258
QY 600 TTACTGAAACTTTTCTACACAAAAGTCAAGATGCATCCACTTACCAATGAAGTGA 659
DB 1259 TTACTGAAACTTTTCTACACAAAAGTCAAGATGCATCCACTTACCAATGAAGTGA 1318
QY 660 CGAGAAATTTACATGTGATAGTACTCTCAGAGAGAGAGTGAACCAAGATATGTCA 719
DB 1319 CGAGAAATTTACATGTGATAGTACTCTCAGAGAGAGAGTGAACCAAGATATGTCA 1378
QY 720 TTCTGGAGGTACCCGGAGCTCATGGGTCTTGGTGTATTTGACCCCTCAGAGTGGAGCAG 779
DB 1379 TTCTGGAGGTACCCGGAGCTCATGGGTCTTGGTGTATTTGACCCCTCAGAGTGGAGCAG 1438
QY 780 CTGTGTTCATGAACTGTGAGAGCTTTTGAACACTGAAAAAGAAAGGTGTGAGACCTA 839
DB 1439 CTGTGTTCATGAACTGTGAGAGCTTTTGAACACTGAAAAAGAAAGGTGTGAGACCTA 1498
QY 840 GAAGAACAAATTTTGTGTTGCAAGCTGGGATGCAAGAAATTTGTCTTCTTGGTTCACTG 899
DB 1499 GAAGAACAAATTTTGTGTTGCAAGCTGGGATGCAAGAAATTTGTCTTCTTGGTTCACTG 1558
QY 900 AGTGGCAGAGATAATTCAGACTCCTTCAAGAGCGTGGCGCTTATATTAATGCTG 959
DB 1559 AGTGGCAGAGATAATTCAGACTCCTTCAAGAGCGTGGCGCTTATATTAATGCTG 1618
QY 960 ACTCATCTATAGAGAACTACACTCTGAGAGTTGATTGTACACCACTGATGTACAGCT 1019

DB 1619 ACTCATCTATAGAGAACTACACTCTGAGAGTTGATTGTATGATACCCGCTGATGTACAGCT 1678
QY 1020 TGGTATTCACACTTACAAAAGAGCTGAAAAGCCCTGATGTAAGGCTTTGAAGGCAATCTC 1079
DB 1679 TGGTATTCACACTTACAAAAGAGCTGAAAAGCCCTGATGTAAGGCTTTGAAGGCAATCTC 1738
QY 1080 TTTATGAAAGTTGGACTAAAAAAGTCTTCCCGAGAGTTCAGTGGCATCCAGAGATAA 1139
DB 1739 TTTATGAAAGTTGGACTAAAAAAGTCTTCCCGAGAGTTCAGTGGCATCCAGAGATAA 1798
QY 1140 GCAAAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCACAGACTTGAATGCTTCAG 1199
DB 1799 GCAAAATTTGGATCTGGAATGATTTTGAAGTGTCTTCCACAGACTTGAATGCTTCAG 1858
QY 1200 GCAGAGCGAGTATCTAAAAAATTTGGAAAAAACAATTCACGCGGTATCCACTGTATC 1259
DB 1859 GCAGAGCGAGTATCTAAAAAATTTGGAAAAAACAATTCACGCGGTATCCACTGTATC 1918
QY 1260 ACAGTGTCTATGAAACATATGAGTGTGGTGAAGGTTTATGATCCCATGTTAAATATC 1319
DB 1919 ACAGTGTCTATGAAACATATGAGTGTGGTGAAGGTTTATGATCCCATGTTAAATATC 1978
QY 1320 ACCTCACTGTGCCAGAGTTGAGAGAGAGTGTGTTGAGCTAGCCAAATTCATAGTGC 1379
DB 1979 ACCTCACTGTGCCAGAGTTGAGAGAGAGTGTGTTGAGCTAGCCAAATTCATAGTGC 2038
QY 1380 TCCCTTTGATGTGCGAGATTTATCTGATTTAAGAAATGCTGCAAAATCTACA 1439
DB 2039 TCCCTTTGATGTGCGAGTATGATGATTTAAGAAATGCTGCAAAATCTACA 2098
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QY 1560 TTGCAAAAACCAACCAATTTGTTAAGAAATGATGATCAACTGATTTCTGGAAA 1619
DB 2219 TTGCAAAAACCAACCAATTTGTTAAGAAATGATGATCAACTGATTTCTGGAAA 2278
QY 1620 GAGCATTTATGATTCATTTAGGTTTACAGACAGACTTTTATAGCATGTCATATG 1679
DB 2279 GAGCATTTATGATTCATTTAGGTTTACAGACAGACTTTTATAGCATGTCATATG 2338
QY 1680 CTCCAAGCAGCCACAACTATGCAAGGAGTCAATTTCCAGAAATTTATGATGCTGT 1739
DB 2339 CTCCAAGCAGCCACAACTATGCAAGGAGTCAATTTCCAGAAATTTATGATGCTGT 2398
QY 1740 TTGATATTTGAAACAAAGTGGACCTTCCAAAGGCTGGGGAGATGTGAAGACAGATT 1799
DB 2399 TTGATATTTGAAACAAAGTGGACCTTCCAAAGGCTGGGGAGATGTGAAGACAGATT 2458
QY 1800 CTGTGGAGCTTTCACAGTGCAGAGACTTCAAGACTTTGAGTGAAGTAAAGAG 1859
DB 2459 ATGTGTGAGCTTTCACAGTGCAGAGACTTCAAGACTTTGAGTGAAGTAAAGAG 2518
QY 1860 ATTCTTATGAGACTCTGTATTTGAATTTGTGTGTATGTCTC- -AAAGATATATATGG 1917
DB 2519 ATTCTTATGAGACTCTGTATTTGAATTTGTGTGTATGTCTC- -AAAGATATATATGG 2578
QY 1918 GTATATTTGATTAATTTTAAATTTGATATTTGAATTAAGTGAATATATATATATAA 1977
DB 2579 GTATATTTGATTAATTTTAAATTTGATATTTGAATTAAGTGAATATATATATATAA 2638
QY 1978 AAAAAAAAAAAAAA 1992
DB 2639 AAAAAAAAAAAAAA 2653

RESULT 7
US-09-978-295A-617

Sequence 617, Application US/09978295A
 Patent No. US20020156006A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kiljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC11
 CURRENT APPLICATION NUMBER: US/09/978, 295A
 PRIOR FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
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 ? PRIOR FILING DATE: 1998-05-15
 ? PRIOR APPLICATION NUMBER: 60/085697

Query Match 84.7% Score 1687.2; DB 10; Length 2558;
 Best Local Similarity 98.6% Pred. No. 0;
 Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

QY 240 AGGTTAAATGCCCCAGCTGGGCGCAAGAGATCTTCTACTAGACCCGTGCTG 299
 DB 821 AGGTTAAATGCCCCAGCTGGGCGCAAGAGATCTTCTACTAGACCCGTGCTG 880
 QY 300 ACTACTTGCTCTGGGGTGAAGTCTCTACGAGCGTGAATCTTCTCGAGGTGCTG 359
 DB 881 ACTACTTGCTCTGGGGTGAAGTCTCTACGAGCGTGAATCTTCTCGAGGTGCTG 940
 QY 360 TCCAGGCTGGAATATCTTAATCTGAATGTGACAGAGACCTCTCACACCGAGTTACC 419
 DB 941 TCCAGGCTGGAATATCTTAATCTGAATGTGACAGAGACCTCTCACACCGAGTTACC 1000
 QY 420 CAGCAATGATACGCTTATAGGATGGAATTGACAGGCTGTGTCTTCCAAATATTC 479

DB 1001 CAGCAATGATACGCTTATAGGCTGGAATTGACAGGCTGTGTCTTCCAAATATTC 1060
 QY 480 CAGTTATCAGCTGATATCTATGATGACAGAGCTCCAGAAAAATGGGTGCTCAG 539
 DB 1061 CAGTTATCAGCTGATATCTATGATGACAGAGCTCCAGAAAAATGGGTGCTCAG 1120
 QY 540 CAGCAGATAGCAGCTGAGAGAGAGTCAAGTGTCTCAATGTTGACCTGCTG 599
 DB 1121 CAGCAGATAGCAGCTGAGAGAGAGTCAAGTGTCTCAATGTTGACCTGCTG 1180
 QY 600 TTACTGGAACCTTTCTACACAAAAAGTCAAGTGCATCCACTCTACCAATGAAGTA 659
 DB 1181 TTACTGGAACCTTTCTACACAAAAAGTCAAGTGCATCCACTCTACCAATGAAGTA 1240
 QY 660 CAGAAATTTACATGATGATAGTACTCTAGAGAGACATGGACACAGATATGCTA 719
 DB 1241 CAGAAATTTACATGATGATAGTACTCTAGAGAGACATGGACACAGATATGCTA 1300
 QY 720 TTCTGGAGGTCCCGGACTCATGGGTGTTGGTGTATTTGACCTCAGAGTGAAGCAG 779
 DB 1301 TTCTGGAGGTCCCGGACTCATGGGTGTTGGTGTATTTGACCTCAGAGTGAAGCAG 1360
 QY 780 CTGTTGTATGAACTGTGAGAGCTTTGGAACACTGAAAAAGAGGCTGAGACCTA 839
 DB 1361 CTGTTGTATGAAATTTGAGAGAGCTTTGGAACACTGAAAAAGAGGCTGAGACCTA 1420
 QY 840 GAAGAACATTTGTTTGAAGCTGGAGTGCACAAATTTGCTCTTCTGTTCTACAG 899
 DB 1421 GAAGAACATTTGTTTGAAGCTGGAGTGCACAAATTTGCTCTTCTGTTCTACAG 1480
 QY 900 AGTGGCAGAGATTAATTAAGACTCTTCAAGAGGTGGCGCTTATTAATTAAGTCG 959
 DB 1481 AGTGGCAGAGATTAATTAAGACTCTTCAAGAGGTGGCGCTTATTAATTAAGTCG 1540
 QY 960 ACTCATCTATGAGAGAACTACACTGTAGAGTTATGTATACACCTGATGTACAGCT 1019
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 QY 1020 TGGTATACAACTTAACAAAGAGCTGAAGAGCTTGAAGGCTTGAAGGAAATCTC 1079
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 QY 1080 TTTATGAAGTTGAGATTAATAAAAGTCTTCCCAAGTTCAGTGCATGCCAGATTA 1139
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OY	1560	TTGCAAAAGCAACCCATATTTGTTAAGATGATGATGATCAACTATGTTCTGCGAA	1619
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Db	2201	GAGCATTTATTTGATCCATTAGGGTTTACCAGACAGCCCTTTTATAGGATGTCAATATG	2260
OY	1680	CTCCAGACGAGCAGACAAAGTATGTCAGGGAGTCATTTCCAGAAATTTATGATGCTCTGT	1739
Db	2261	CTCCAGACGAGCAGACAAAGTATGTCAGGGAGTCATTTCCAGAAATTTATGATGCTCTGT	2320
OY	1740	TTGATATTGGAAGCAAGTGGACCCCTTCCAGGCGCTGGGGAGATGTGAAGAGACAGATT	1799
Db	2321	TTTGATATTGGAAGCAAGTGGACCCCTTCCAGGCGCTGGGGAGAGTGAAGAGACAGATT	2380
OY	1800	CTGTATTCAGCCTTCACAGTGCAGCAGCGTCGAGAGACTTTAGTGAATACCTTAAGAG	1859
Db	2381	ATGTTCAGCCTTCACAGTGCAGCAGCGTCGAGAGACTTTAGTGAATACCTTAAGAG	2440
OY	1860	ATTCCTTTAGAGACTCTGTATTGAAATTTTGTTGTTGATGTCACTC--AAAGAAATTAATGG	1917
Db	2441	ATTTTTTAGAGAAATCCGATGATGAAATTTTGTTGTTGATGTCACTCAGAAAGAAATCGAAATGG	2500
OY	1918	GTAATATTCATATAATTTTAAAAATGGATATTTTGAATTAAGTGAATTTTATATATA	1975
Db	2501	GTAATATTCATATAATTTTAAAAATGGATATTTTGAATTAAGTGAATTTTATATATA	2558

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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 84.7%; Score 1687.2; DB 10; Length 2558;
 Best Local Similarity 98.6%; Pred. No. 0;
 Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

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 Db 941 TCCAGCGTGAATATCTCTAATCTGAATGTCAGAGACCTCTCACACGATTACC 1000
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 QY 420 CAGCAATGATATGCTTTATAGCATGAATGTCAGAGCTGTGGCTTCCAGATTC 479
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 Db 1001 CAGCAATGATATGCTTTATAGCATGAATGTCAGAGCTGTGGCTTCCAGATTC 1060
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 Db 1061 CTGTTATCATCGATTGATATGATGACAGAGCTCTAGAAAAATGGTGGCTCAG 1120
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OY 1140 GCAAAATGGGATCGGAAATGATTTTGAAGGTTCTTCCCAAGCACTTGGAAATGCTCTAG 1139
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OY 1200 GCAGAGCAGCGTATACATAAAATTTGGAAACAACAATTCAGCGCTATCCACTGATC 1259
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OY 1918 GATATTTGATTAATTTTAAATTTGATATTTGAATTAAGTGAATTTATATATAA 1975
Db 2501 GATATTTGATTAATTTTAAATTTGATATTTGAATTAAGTGAATTTATATATAA 2558

RESULT 9
US-09-978-192A-617
Sequence 617, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
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44 PRIOR FILING DATE: 1998-05-15
45 PRIOR APPLICATION NUMBER: 60/085697

Query Match 84.7%; Score 1687.2; DB 10; Length 2558;

Best Local Similarity 98.6%; Pred. No. 0; Mismatches 23; Indels 2; Gaps 1;

Matches 1713; Conservative 0;

QY 240 AGGTTAAATGCGCCAGCTGCGAGGGCCAAAGAGTCATTCTCTACGACCGCTGCG 239
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QY 300 ACTACTTGTGCTCTGCGGGTGAAGTCTTATCCAGACGCTTGAATCTTCTGAGGTGCG 359
DB 881 ACTACTTGTGCTCTGCGGGTGAAGTCTTATCCAGACGCTTGAATCTTCTGAGGTGCG 940
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DB 941 TCCAGCGTGAATATCTTAATCTGAATGTCGAGAGACCTCTCACACGAGTTACC 1000
QY 420 CAGCAATGATGCGTTTATGCGATGGAATGTCAGAGCGTGTGCTTCCAGATATTC 479
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; Sequence 617, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavira, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FIDE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999, 832A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641

[illegible]

;; PRIOR FILING DATE: 1998-05-15
 ;; PRIOR APPLICATION NUMBER: 60/085704
 ;; PRIOR FILING DATE: 1998-05-15
 ;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 84.7% Score 1687.2; DB 10; Length 2558;
 Best Local Similarity 98.6%; Pred. No. 0;
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DB 821 AGGTTAAATAGCCAGCTGGCAGGGCCAAAGAGCATTCCTCTACTCAGACCCCTGCTG 880
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QY 300 ACTACTTTCCTCTGGGGTGAAGTCTATCCAGACGGTTGGAACTTCTCTGGAGTGGTG 359
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DB 881 ACTACTTTCCTCTGGGGTGAAGTCTATCCAGACGGTTGGAACTTCTCTGGAGTGGTG 940
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QY 360 TCCAGCGTGAATATCTCTAAATCTGAATGTCAGAGACCTCTCAGACCCAGTTACC 419
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DB 941 TCCAGCGTGAATATCTCTAAATCTGAATGTCAGAGACCTCTCAGACCCAGTTACC 1000
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QY 420 CAGCAATGATAGCGCTTATAGCGATGGAATTCAGAGCGCTGTGCTTCCAAAGTATTC 479
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QY 480 CTGTTTCATCCAGTTGATCTATGATGACAGAGAGCTCTCTAGAAAAATGGGTGGCTCAG 539
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DB 1061 CTGTTTCATCCAGTTGATCTATGATGACAGAGAGCTCTCTAGAAAAATGGGTGGCTCAG 1120
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QY 540 CACCAACCGATAGACGCTGGAGAGAGAGTCTCAAAAGTCTCTACAATTTGGACCTGGCT 599
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DB 1121 CACCAACCGATAGACGCTGGAGAGAGAGTCTCAAAAGTCTCTACAATTTGGACCTGGCT 1180
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DB 1241 CGAGAAATTTACAAATGATGATAGTACTCTCAGAGAGAGAGTGGAAACAGATATGTC 1300
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DB 1301 TTCTGGAGGCTACCGGGACATCATGGGTGTTGGTGATATGACCTCTCAGAGTGGAGAG 1360
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DB 1361 CTGTTTCATGAAACCTGTGAGAGCTTTGGAACACTGAAAAAGAGAGGTGGAGACCTA 1420
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QY 1800 CTGTTGCAAGCTTTCACAGTGGCAGGCTGTCAGAGACTTTGATGAAGTGAAGTGAAGTGAAG 1859
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RESULT 11

US-09-978-189-617

Sequence 617, Application US/09978189

Publication No. US20030004102A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi
 ;; APPLICANT: Baker Kevin P.
 ;; APPLICANT: Botstein, David
 ;; APPLICANT: Desnoyers, Luc
 ;; APPLICANT: Eaton, Dan
 ;; APPLICANT: Ferrara, Napoleon
 ;; APPLICANT: Filvaroff, Ellen
 ;; APPLICANT: Fond, Sherman
 ;; APPLICANT: Geo, Wei-Qiang
 ;; APPLICANT: Geiber, Hanspeter
 ;; APPLICANT: Gerlitsen, Mary E.
 ;; APPLICANT: Goddard, Audrey
 ;; APPLICANT: Godowski, Paul J.
 ;; APPLICANT: Grimaldi, J. Christopher
 ;; APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James;
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C7
 CURRENT APPLICATION NUMBER: US/09/978,189
 PRIOR APPLICATION NUMBER: 2001-10-15
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24 PRIOR APPLICATION NUMBER: 60/085700
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33 PRIOR FILING DATE: 1998-05-15
34 PRIOR APPLICATION NUMBER: 60/085704
35 PRIOR FILING DATE: 1998-05-15
36 PRIOR APPLICATION NUMBER: 60/085697

Query Match 84.7%; Score 1687.2; DB 11; Length 2558;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

QY 240 AGGTTAAATGCCAGCTGGCAGGGCCAAAGAGTCATCTCTACTCAGACCTGCTG 299
DB 821 AGGTTAAATGCCAGCTGGCAGGGCCAAAGAGTCATCTCTACTCAGACCTGCTG 880
QY 300 ACTACTTGTCTCGGGGTGAAGTCTATCCAGACGGTTGAATCTTCTGAGAGTGTG 359
DB 881 ACTACTTGTCTCGGGGTGAAGTCTATCCAGACGGTTGAATCTTCTGAGAGTGTG 940
QY 360 TCCAGCGTGAATATCTTAATCTGAATGTGTGACAGACCTCTCACACAGGTTACC 419
DB 941 TCCAGCGTGAATATCTTAATCTGAATGTGTGACAGACCTCTCACACAGGTTACC 1000
QY 420 CAGCAATGATACGCTTATAGCGATGGAATTCGAGAGGCTGTGCTTCCAAATATC 479
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DB 1061 CTGTTTATCAGTTGGATCTATGATGACAGAAAGCTCTTGAATAATGGGTGCTAG 1120
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QY 1320 ACCTCAGTGTGAGCCAGGATTCAGAGAGAGATGTGTTGAGCTAGCCAAATTCATGTGC 1379
DB 1901 ACCTCAGTGTGAGCCAGGATTCAGAGAGAGATGTGTTGAGCTAGCCAAATTCATGTGC 1960
QY 1380 TCCCTTTTGTATGCGAGATTAATGCTGTATTTTAAAGATATGTCACAAAATCTACA 1439
DB 1961 TCCCTTTTGTATGCGAGATTAATGCTGTATTTTAAAGATATGTCACAAAATCTACA 2020
QY 1440 ATATTTCATGAACATCCACAGAAATGAAGATACAGTTCATTTGATTCACCTTT 1499
DB 2021 GTATTTTCATGAACATCCACAGAAATGAAGATACAGTTCATTTGATTCACCTTT 2080
QY 1500 TTTCTGCAATTAATTTTACAGAAATGCTTCCAAAGTTCAGGAGAGATCCAGACT 1559
DB 2081 TTTCTGCAATTAATTTTACAGAAATGCTTCCAAAGTTCAGGAGAGATCCAGACT 2140
QY 1560 TTGACAAAAGCAACCAATATGATTAAGAAATGAAGATGATCAATGATTTCTGAAA 1619
DB 2141 TTGACAAAAGCAACCAATATGATTAAGAAATGAAGATGATCAATGATTTCTGAAA 2200
QY 1620 GAGCATTTATGATCCATTTAGGTTTACAGACACACTTTTATAGGATGTCTATG 1679
DB 2201 GAGCATTTATGATCCATTTAGGTTTACAGACACACTTTTATAGGATGTCTATG 2260
QY 1680 CTCCAGAGCAGCAACAAGATATCAGGGAGTATTCAGAGAAATTTATGATGCTGT 1739
DB 2261 CTCCAGAGCAGCAACAAGATATCAGGGAGTATTCAGAGAAATTTATGATGCTGT 2320
QY 1740 TTGATATTTGAAGCAAGTGGACCTTCCAGGCTGGGAGATGTGAAGACAGATTT 1799
DB 2321 TTGATATTTGAAGCAAGTGGACCTTCCAGGCTGGGAGATGTGAAGACAGATTT 2380
QY 1800 CTGTTGACGCTTTCACAGTGTGACAGCTGTGACAGACTTTGATGTAAGTACCTTAAGAG 1859

Db 2381 ATGTTGCAGCCTTACACAGTGCAGGCAGCTGCAGACACTTTAGTGAAGTACCTTACAGAGG 2440

Oy 1860 ATTCCTTAGACACTCTGTATTGAATTTGTGTGTATGTCACTC--AAAGAATAATAATGG 1917

Db 2441 ATTTTGTAGAAATCCGATGATGAATTTGTGTGTATGTCACTCAGAAAGATCGTAATGG 2500

Oy 1918 GTATATTGATTAATTTTAAATTTGATATTATTGAATTAAGTTGAATTTTATATATA 1975

Db 2501 GTATATTGATTAATTTTAAATTTGATATTATTGAATTAAGTTGAATTTTATATATA 2558

RESULT 12
US-09-978-608A-617

; Sequence 617, Application US/09978608A
; Publication No. US20030045462A1

```

: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J
: APPLICANT: Kijavrin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James;
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2630PIC22
: CURRENT APPLICATION NUMBER: US/09/978,608A
: CURRENT FILING DATE: 2001-10-16
: NUMBER OF SEQ ID NOS: 624
: Prior Application removed - See File Wrapper or Palm
: SEQ ID NO 617
: LENGTH: 2558
: TYPE: DNA
: ORGANISM: Homo Sapien
: OS-09-978-608A-617

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Query Match	84.7%;	Score 1687.2;	DB 11;	Length 2558;
Best Local Similarity	98.68;	Pred. No. 0;		
Matches 1713; Conservative	0;	Mismatches 23;	Indels 2;	Gaps 1.

[illegible]

QY	420	CAGCAAAATGAATACCCCTTATATAGGCATGCAATTTGCAGAGGCTGTTGGTCTTCCAAAGTATTC	479
Db	1001	CAGCAAAATGAATATGCTTATATAGGGCTGGAAATTGCAGAGGCTGTTGGTCTTCCAAAGTATTC	1060
QY	480	CTGTTTCATCCAGTTGGATGACTATAGTGCACAGAAAGCTCTGAAAAATATGGGTGGCTCAG	539
Db	1061	CTGTTTCATCCAAATTTGGATGACTATATGTCACAGAAAGCTCTGAAAAATATGGGTGGCTCAG	1120
QY	540	CACCAACAGATAGCAGCTGAGAGAGAACTCCAAGTGTCCCTACAAATGTTGGACCTGGCT	599
Db	1121	CACCAACAGATAGCAGCTGAGAGAGAACTCCAAGTGTCCCTACAAATGTTGGACCTGGCT	1180
QY	600	TTACTGGAACCTTTCTATACAAAAAGTCAAGATGACATCCACTCTACATGAAGTGA	659
Db	1181	TTACTGGAACCTTTCTACAAAAAGTCAAGATGACATCCACTCTACATGAAGTGA	1240
QY	660	CGAGAAATTACAAATGTGATAGTACTCTCAGAGAGCAGAGTGGAAACCGACAGATATGTCA	719
Db	1241	CGAGAAATTACAAATGTGATAGTACTCTCAGAGAGCAGAGTGGAAACCGACAGATATGTCA	1300
QY	720	TTCTGAGAGTCACCGGAGCTCATGGGCTGTTGGTGGATTTGACCCTCAGAGTGGAGCAG	779
Db	1301	TTCTGAGAGTCACCGGAGCTCATGGGCTTGGTGGATTTGACCCTCAGAGTGGAGCAG	1360
QY	780	CTGTTGTTTCATGAACACTGTGAGAGCTTTGGAACACTGAAAAAGAGGCTGAGACTTA	839
Db	1361	CTGTTGTTTCATGAAAAATGTGAGAGCTTTGGAACACTGAAAAAGAGGCTGAGACTTA	1420
QY	840	GAAAGAACAAATTTGTTGCCAAGCTGGGATGCGAAGAAATTTGGCTCTTGTTGTTCTACTG	899
Db	1421	GAAAGAACAAATTTGTTGCCAAGCTGGGATGCGAAGAAATTTGGCTCTTGTTGTTCTACTG	1480
QY	900	AGTGGGCGAGAGATTAATCAAGACTCCCTCAAGAGCGTGGCTGATATATTAATCCTG	959
Db	1481	AGTGGGCGAGAGAGATTCAGAGACTCCCTCAAGAGCGTGGCTGATATTAATGCTG	1540
QY	960	ACTCATCTATAGAAAGAAACTACACTGTGAGATTTGATTTGACACCACTGATGTACAGCT	1019
Db	1541	ACTCATCTATAGAAAGAAACTACACTGTGAGATTTGATTTGACACCCGCTGATGTACAGCT	1600
QY	1020	TGCTATACAACTTAACAAAGAGCTGMAAAACCCCTGATGAAGGCTTTGAAGCAAACTC	1079
Db	1601	TGCTATACAACTTAACAAAGAGCTGMAAAACCCCTGATGAAGGCTTTGAAGCAAACTC	1660
QY	1080	TTTATGAAGTTGGACTTAAAAAAAGTCCCTCCAGAGTTAGTGGCATGCCAGAGATTA	1139
Db	1661	TTTATGAAGTTGGACTTAAAAAAAGTCCCTCCAGAGTTAGTGGCATGCCAGAGATTA	1720
QY	1140	GCAAAATTTGGATCTGGAATATGATTTGAGTGTCTTCCAAAGCATTTGGAATGCTCTCAG	1199
Db	1721	GCAAAATTTGGATCTGGAATATGATTTGAGTGTCTTCCAAAGCATTTGGAATGCTCTCAG	1780
QY	1200	GCAGAGCAGGCTATACATAAATTTGGGAAACAAACAAATTCAGGGGCTATCCACTGATC	1259
Db	1781	GCAGAGCAGGCTATACATAAATTTGGGAAACAAACAAATTCAGGGGCTATCCACTGATC	1840
QY	1260	ACAGTGTATGAACAAATATGATGTTGGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1319
Db	1841	ACAGTGTATGAACAAATATGATGTTGGGAAAAAGTTTATGATCCAAATGTTTAAATATC	1900
QY	1320	ACCTCACTGTGGCCCGAGTCTGAGAGAGGATGTGTTGAGCTAGGCCAATTCATAGTGC	1379
Db	1901	ACCTCACTGTGGCCCGAGTCTGAGAGAGGATGTGTTGAGCTAGGCCAATTCATAGTGC	1960
QY	1380	TCCCTTTTGATTTGTCGAAATATATGCTGTAGTTTAAAGAAATATGCTGACAAATCTACA	1439
Db	1961	TCCCTTTTGATTTGTCGAAATATATGCTGTAGTTTAAAGAAATATGCTGACAAATCTACA	2020
QY	1440	ATATTTTCATGAACATCCACAGAAATGAAGCATACAGTTTATTCATTTGATTCACCTT	1499
Db	2021	ATATTTTCATGAACATCCACAGAAATGAAGCATATACAGTATTCATTTGATTCACCTT	2080
QY	1500	TTTCTGCGAGTAAAAATTTTACAGAAATTTGCTTCCAAAGTTCCAGCAGAGATCCGAGACT	1559

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Db      2081  TTTCTGAGTAAAGAAATTTTACAGAAATGCTTCCAAAGTTCAGAGAGAGCTCCAGAGCT 2140
Oy      1560  TTGACAAAGACCAACCAATATTTTAAAGATGATGATGATCACTCATGTTCTGAGAA 1619
Db      2141  TTGCAAAAGACCAACCAATATTTTAAAGATGATGATGATCACTCATGTTCTGAGAA 2200
Oy      1620  GAGCATTTTATGATTCATTTAGGGTTTACACAGACACTTTTATAGGCATGTCATATG 1679
Db      2201  GAGCATTTTATGATTCATTTAGGGTTTACACAGAGCCCTTTTATAGGCATGTCATATG 2260
Oy      1680  CTCCACAGCCCAACAAAGATATGACAGGGAGTCATTTCCCGAATTTATATGCTCTGT 1739
Db      2261  CTCCACAGCCCAACAAAGATATGACAGGGAGTCATTTCCCGAATTTATATGCTCTGT 2320
Oy      1740  TTGATTTTGAAGAAAGTGGAGCCCTTCCAGAGCCCTGGGAGAGATGTGAAGAGAGATTT 1799
Db      2321  TTGATTTTGAAGAAAGTGGAGCCCTTCCAGAGCCCTGGGAGAGATGTGAAGAGAGATTT 2380
Oy      1800  CTGTTGACGCTTACAGAGTGCAGAGCTGCAGAGACTTTGATGAGATGACCTTAAGAG 1859
Db      2381  ATGTTGACGCTTACAGAGTGCAGAGCTGCAGAGACTTTGATGAGATGACCTTAAGAG 2440
Oy      1860  ATCTTTAGAGCTCTGATGATGATTTGTTGTTGATGTCATCTC--AAAGATTAATATG 1917
Db      2441  ATTTTTTGAAGAAATCCGATTTGAAATTTGTGTGTATGTCTACAGAAAGAAATGTA 2500
Oy      1918  GTATTTGATTAATTTTAAATTTGTAATTTTGAATTTTGAATTTTATATATA 1975
Db      2501  GTATTTGATTAATTTTAAATTTGTAATTTTGAATTTTGAATTTTATATATA 2558

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RESULT 13

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US-09-978-585A-617
: Sequence 617, Application US/09978585A
: Publication No. US20030049633A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Kuo, Sophia S.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630pic15
: CURRENT APPLICATION NUMBER: US/09/978,585A
: NUMBER OF SEQ ID NOS: 624
: Prior Application removed - See File Wrapper or Palm
: SEQ ID NO 617
: LENGTH: 2556

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: TYPE: DNA
: ORGANISM: Homo Sapien
: US-09-978-585A-617
Query Match      84.7%; Score 1687.2; DB 11; Length 2556;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

Oy      240  AGGTTAAAGATGCCAGCTGGCAGGGCCAAAGAGTCTCTACTCAGACCCCTCTG 299
Db      821  AGGTTAAAGATGCCAGCTGGCAGGGCCAAAGAGTCTCTACTCAGACCCCTCTG 880
Oy      300  ACTACTTGTCCCTGGGGGTGAAGTCATTCAGAGGGTTGGAAATCTTCTGAGAGTGTG 359
Db      881  ACTACTTGTCCCTGGGGGTGAAGTCATTCAGAGGGTTGGAAATCTTCTGAGAGTGTG 940
Oy      360  TCCAGCGTGAAGATATCTAAATCTGAATGTGACAGAGACCCCTCAGACAGAGTTACC 419
Db      941  TCCAGCGTGAAGATATCTAAATCTGAATGTGACAGAGACCCCTCAGACAGAGTTACC 1000
Oy      420  CAGCAATGATATACGCTTATAGCATGGAATTCAGAGGCTGTGTCTTCCAAAGTATTC 479
Db      1001  CAGCAATGATATATGCTTATAGGCGTGAATTCAGAGGCGTGTGTCTTCCAAAGTATTC 1060
Oy      480  CTGTTCAATCCAGTTGATATGATGATGACAGAGAGTCCCTAGAAATAATGGGTGCTCAG 539
Db      1061  CTGTTCAATCCAGTTGATATGATGATGACAGAGAGTCCCTAGAAATAATGGGTGCTCAG 1120
Oy      540  CACCACAGATAGCAGCTGAGAGAGAGTCTCAAGTGTCTTACATATGTTGACCTGCT 599
Db      1121  CACCACAGATAGCAGCTGAGAGAGAGTCTCAAGTGTCTTACATATGTTGACCTGCT 1180
Oy      600  TTACTGCAACTTTTCTACACAAAAGTCAAGATGACATCCACTTCAATGAATGA 659
Db      1181  TTACTGCAACTTTTCTACACAAAAGTCAAGATGACATCCACTTCAATGAATGA 1240
Oy      660  CGAATAATTCAATGTGTATGATGATCTCTCAGAGAGAGTGAACACAGATATGTCA 719
Db      1241  CGAATAATTCAATGTGTATGATGATCTCTCAGAGAGAGTGAACACAGATATGTCA 1300
Oy      720  TTCTGGAGAGTCCACGGGACTCATGGGTGTTGGTGTATTTGACCTCAGAGTGGACAG 779
Db      1301  TTCTGGAGAGTCCACGGGACTCATGGGTGTTGGTGTATTTGACCTCAGAGTGGACAG 1360
Oy      780  CTGTTGTTCAATGAAGTGTGAGAGCTTTGGAACATGAAAAGAAAGCGTGGAGACCTA 839
Db      1361  CTGTTGTTCAATGAAGTGTGAGAGCTTTGGAACATGAAAAGAAAGCGTGGAGACCTA 1420
Oy      840  GAAGAACAAATTTGTTTCAAGCTGGAGTGCAGAAATTTGTTGTTCTTCTACTG 899
Db      1421  GAAGAACAAATTTGTTTCAAGCTGGAGTGCAGAAATTTGTTGTTCTTCTACTG 1480
Oy      900  AGTGGGACAGAGATTAATCAAGACTCCTTCAAGAGCTGGCGTGGCTTATTTATGCTG 959
Db      1481  AGTGGGACAGAGATTAATCAAGACTCCTTCAAGAGCTGGCGTGGCTTATTTATGCTG 1540
Oy      960  ACTCATCTATGAGAGAACTACACTCTGAGAGTTGATTTACCCACTGATGTACAGCT 1019
Db      1541  ACTCATCTATGAGAGAACTACACTCTGAGAGTTGATTTACCCACTGATGTACAGCT 1600
Oy      1020  TGGTATACACCTTAACAAAGAGTGAAGAGCCCTGATGAAGGCTTTGAAAGCAATCTC 1079
Db      1601  TGGTATACACCTTAACAAAGAGTGAAGAGCCCTGATGAAGGCTTTGAAAGCAATCTC 1660
Oy      1080  TTTATGAAGTGTGACATTAAGAAAGTCTTCCCGAGAGTCAAGTGCATGCCAGAGTAA 1139
Db      1661  TTTATGAAGTGTGACATTAAGAAAGTCTTCCCGAGAGTCAAGTGCATGCCAGAGTAA 1720
Oy      1140  GCAATTTGGATCTGGAATATGTTTGAAGGTGTTCTTCCAGAGATTTGGAATTTGCTAG 1199
Db      1721  GCAATTTGGATCTGGAATATGTTTGAAGGTGTTCTTCCAGAGATTTGGAATTTGCTAG 1780
Oy      1200  GCAGAGCAGCGTATCTAATAAATTTGGAACAAACAAATTCAGCGGTATCCACTGTATC 1259

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Db 1781 GCAGAGCAGCGTATCTAATAAATGGCAACAAACAAATTCAGGGCTATCCACTGATC 1840
QY 1260 ACAGTCTCTATGAAACATATAGTGTGTGAAAAAGTTTATGATCCATGTTTAAATATC 1319
Db 1841 ACAGTCTCTATGAAACATATAGTGTGTGAAAAAGTTTATGATCCATGTTTAAATATC 1900
QY 1320 ACCGCACTGTGGCCAGGTTCGAGAGGAGGTGGTTTGAGTCAGCAATTCATAGTGC 1379
Db 1901 ACCGCACTGTGGCCAGGTTCGAGAGGAGGTGGTTTGAGTCAGCAATTCATAGTGC 1960
QY 1380 TCCCTTTGATGTGCGATTAATGCTGTAGCTTTTAAAGAAATGCTGACAAATCTACA 1439
Db 1961 TCCCTTTGATGTGCGATTAATGCTGTAGCTTTTAAAGAAATGCTGACAAATCTACA 2020
QY 1440 ATATTTCTATGAAACATCCACAGAAATGAAGACATACATTTATCTATTTGATTCATT 1499
Db 2021 GTATTTCTATGAAACATCCACAGAAATGAAGACATACATTTATCTATTTGATTCATT 2080
QY 1500 TTTCTGAGTAAATAATTTTACAGAAATGCTTCCAGTTCAGCGAGAGCTCCAGACT 1559
Db 2081 TTTCTGAGTAAATAATTTTACAGAAATGCTTCCAGTTCAGCGAGAGCTCCAGACT 2140
QY 1560 TTGACAAAAGCAACCAATATGTTTAAAGAAATGAATGATCAACTCATGTTCTGAAA 1619
Db 2141 TTGACAAAAGCAACCAATATGTTTAAAGAAATGAATGATCAACTCATGTTCTGAAA 2200
QY 1620 GACGATTTATGATTCATTTAGGTTTACAGAGAGCTTTTATAGCATATCTATG 1679
Db 2201 GACGATTTATGATTCATTTAGGTTTACAGAGAGCTTTTATAGCATATCTATG 2260
QY 1680 CTCGACGAGCCACACAAATATGTCAGAGGAGTCATTCAGGAAATTTATGATGCTGT 1739
Db 2261 CTCGACGAGCCACACAAATATGTCAGAGGAGTCATTCAGGAAATTTATGATGCTGT 2320
QY 1740 TTGATATGAAACAAAGTGACCTTCCAGGCTGGGGAGATGTGAAGACAGATTT 1799
Db 2321 TTGATATGAAACAAAGTGACCTTCCAGGCTGGGGAGATGTGAAGACAGATTT 2380
QY 1800 CTGTCGAGCCCTTCAGAGTCAGGAGGAGCTTCAGAGACTTTGATGAAGTGCCTAAGAG 1859
Db 2381 ATGTTGAGCCCTTCAGAGTCAGGAGGAGCTTCAGAGACTTTGATGAAGTGCCTAAGAG 2440
QY 1860 ATGTTGAGAGCTCTGTATGATTTGTTGTGTATGTCACCTC - AAAGATATATATG 1917
Db 2441 ATTTTATGAGATTCCTATGATTTGTGTGTATGTCACCTCAGAAAGATGCTATG 2500
QY 1918 GTATATGATTAATTTTAAATTTGATATTTGAAATTAAGTTGAATATATATATA 1975
Db 2501 GTATATGATTAATTTTAAATTTGATATTTGAAATTAAGTTGAATATATATATA 2558

RESULT 14
US-09-978-191A-617
; Sequence 617, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
```

```

; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978, 191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
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Db 1301 TTCTGGAGGTACCCGGAGCTCATGGGTGTTGGTGTATGACCTTCAGAGGAGCAG 1360
QY 780 CTGTTGTACGAAAGTGGAGAGCTTTGGAAACATGAAAAAGAGGTGGAGACCTA 839
Db 1361 CTGTTGTACGAAAGTGGAGAGCTTTGGAAACATGAAAAAGAGGTGGAGACCTA 1420
QY 840 GAAGAACAAATTTGTTGGAGCTGGAGTGCAGAGAAATTTGGTCTCTTGGTTCTACTG 899
Db 1421 GAAGAACAAATTTGTTGGAGCTGGAGTGCAGAGAAATTTGGTCTCTTGGTTCTACTG 1480
QY 900 AGTGGCAGAGATTAATTCAGACTCTTCAGAGCGTGGCGTGTATATATATGCTG 959
Db 1481 AGTGGCAGAGAGAAATTCAGACTCTTCAGAGCGTGGCGTGTATATATATGCTG 1540
QY 960 ACATCATATAGAGAGAACTACACTGTAGAGTTATGTACACACGATGATACAGCT 1019
Db 1541 ACTCATCTATAGAGAGAACTACACTGTAGAGTTATGTACACACGATGATACAGCT 1600
QY 1020 TGGTATACAACTTAACAAAGAGCTGAAAAAGCCCTGATGAAGCTTTGAAGCAATCTC 1079
Db 1601 TGGTATACAACTTAACAAAGAGCTGAAAAAGCCCTGATGAAGCTTTGAAGCAATCTC 1660
QY 1080 TTTATGAAGTGGACTAAAAAAGTCTCCAGAGTTCAGTGCATGCCAGAGATAA 1139
Db 1661 TTTATGAAGTGGACTAAAAAAGTCTCCAGAGTTCAGTGCATGCCAGAGATAA 1720
QY 1140 GCAAAATGGAGTCTGAAATGATTTGAGTGTCTTCCAGAGACTTGGAAATGGCTCAG 1199
Db 1721 GCAAAATGGAGTCTGAAATGATTTGAGTGTCTTCCAGAGACTTGGAAATGGCTCAG 1780
QY 1200 GCAGAGCAGGTATACATAAAATTTGGAAAAACAATAACAGCGCTATCCACTGTATC 1259
Db 1781 GCAGAGCAGGTATACATAAAATTTGGAAAAACAATAACAGCGCTATCCACTGTATC 1840
QY 1260 ACAGTGTCTATGAACATATGAGTTGGTGGAAAAAGTTTATGATCCAAATGTTTAAATATC 1319
Db 1841 ACAGTGTCTATGAACATATGAGTTGGTGGAAAAAGTTTATGATCCAAATGTTTAAATATC 1900
QY 1320 ACTCTACGTGGGCCGAGTTCGAGAGGGAGTGTGTTAGCTAGCATTCCATGCTGC 1379
Db 1901 ACTCTACGTGGGCCGAGTTCGAGAGGGAGTGTGTTAGCTAGCATTCCATGCTGC 1960
QY 1380 TCCCTTTGATTTGTCAGATTAATGCTGTAGTTTAAAGAAATGCTGCAAAATCTACA 1439
Db 1961 TCCCTTTGATTTGTCAGATTAATGCTGTAGTTTAAAGAAATGCTGCAAAATCTACA 2020
QY 1440 ATATTTCTATGAACATCTCACAGAGAAATGAGACATACAGTTTATCATTTGATTCCTT 1499
Db 2021 ATATTTCTATGAACATCTCACAGAGAAATGAGACATACAGTTTATCATTTGATTCCTT 2080
QY 1500 TTTTGCAGTAAAAAATTTTACAGAAATGCTCCAGTTCAGCGGAGACATCCAGAGAT 1559
Db 2081 TTTTGCAGTAAAAAATTTTACAGAAATGCTCCAGTTCAGCGGAGACATCCAGAGAT 2140
QY 1560 TTGACAAAAGCAACCAATATTGTTAAGATGATGATGATCAACTAGCTTTCTGGAAA 1619
Db 2141 TTGACAAAAGCAACCAATATTGTTAAGATGATGATGATCAACTAGCTTTCTGGAAA 2200
QY 1620 GAGCATTTATGATTCATTAGGCTTACACAGACAGACTTTTATATAGCATGTCTATG 1679
Db 2201 GAGCATTTATGATTCATTAGGCTTACACAGACAGACTTTTATATAGCATGTCTATG 2260
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RESULT 15
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; Sequence 617, Application US/09978403A
; Publication No. US20030050240A1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fonq, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978, 403A
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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Query Match 84.7%; Score 1687.2; DB 11; Length 2558;
 Best Local Similarity 98.6%; Pred. No. 0;
 Matches 1713; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	2288	98.2	750	10	US-09-895-793-944
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16	2288	98.2	750	11	US-09-918-585A-618	Sequence 618, App
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ALIGNMENTS

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; Sequence 944, Application us/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FASTSEQ for Windows version 3.0
; SEQ ID NO 944
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-822-827-944

Query Match 98.2%; Score 2288; DA 9; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;

Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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RESULT 2
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Sequence 618, Application US/09978295A
Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978, 295A
CURRENT FILING DATE: 2001-10-15
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085697
Query Match 98.2%; Score 2288; DB 10; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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DB 309 MGSAPPDSSMRGSLKYPVWVGPGFTGNFSTQVKMHISTNEVTRIVNYIGTLRGAVEP 368
QY 61 DRYVILGGHRDVSFVGIDPQGAAYVHETVRSFGTLKKEGMPRRRTILFASWDAEBFGL 120
DB 369 DRYVILGGHRDVSFVGIDPQGAAYVHETVRSFGTLKKEGMPRRRTILFASWDAEBFGL 428
QY 121 LGSTEWAEDNSRLIOEGVAVYNADSSIEGNYLTRDCCPLMTSLVHNLTKEKSPDEGP 180
DB 429 LGSTEWAEDNSRLIOEGVAVYNADSSIEGNYLTRDCCPLMTSLVHNLTKEKSPDEGP 488
QY 181 EGSLSYESTWTKSPSPESFGMPRISKLGSNDPEVEFFORLGIASGRARYTKMNETKPSG 240
DB 489 EGSLSYESTWTKSPSPESFGMPRISKLGSNDPEVEFFORLGIASGRARYTKMNETKPSG 548
QY 241 YPLYSYETTELVEKRYDPMFKYHLTVAOVRCGMVPELANSTVLPDCCRDAVAVLRKTA 300
DB 549 YPLYSYETTELVEKRYDPMFKYHLTVAOVRCGMVPELANSTVLPDCCRDAVAVLRKTA 608
QY 301 DKTYNISMKHPQEMKTYSLSFDSLFAVKNFTETIAKFSRLODPKSNPILRMNNDOL 360
DB 609 DKTYNISMKHPQEMKTYSLSFDSLFAVKNFTETIAKFSRLODPKSNPILRMNNDOL 668
QY 361 MFLERAFIDPLGDPDPPEFYHVHYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAMGV 420
DB 669 MFLERAFIDPLGDPDPPEFYHVHYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAMGV 728
QY 421 KROIYVAFTVQAAETLSEVA 442
DB 729 KROIYVAFTVQAAETLSEVA 750
RESULT 3
US-09-978-697-618
Sequence 618, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630PLC27
CURRENT APPLICATION NUMBER: US/09/978.697
CURRENT FILING DATE: 2001-10-16
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Query Match 98.2%; Score 2288; DB 10; Length 750;
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 Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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RESULT 4
 US-09-978-192A-618
 Sequence 618, Application US/09978192A
 Patent No. US20020177553A1

GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
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 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC9
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 CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
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PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
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PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2%; Score 2288; DB 10; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPPDSSWRGSLKSYNVGPGFTGNFSTOKVKMHIHSTNEVTRIYNYIGTLRGAVEP 60
DB 309 MGSAPPDSSWRGSLKPYNVGPGFTGNFSTOKVKMHIHSTNEVTRIYNYIGTLRGAVEP 368
QY 61 DRYVILGHRDSWFGGIDPOSSGAAYVHEVYRSFGTLKKGWRRRTIILASMDAEFGL 120
DB 369 DRYVILGHRDSWFGGIDPOSSGAAYVHEVYRSFGTLKKGWRRRTIILASMDAEFGL 428
QY 121 LGSTEMAEDNSRLQEGVAYINADSSIEGNYTLRVCTPLMYSLVNLTRELKSPDEGF 180
DB 429 LGSTEMAEDNSRLQEGVAYINADSSIEGNYTLRVCTPLMYSLVNLTRELKSPDEGF 488
QY 429 LGSTEMAEDNSRLQEGVAYINADSSIEGNYTLRVCTPLMYSLVNLTRELKSPDEGF 488
DB 181 EGKSLYESWTKRSPSPFGMPRIKLSGNDPEVFQRLGIASGRARYTKNMTNFKFSG 240
QY 489 EGKSLYESWTKRSPSPFGMPRIKLSGNDPEVFQRLGIASGRARYTKNMTNFKFSG 548
DB 241 YPLVHSYETVELYERKYDDPMFKHLVLAQVYRGAMVELANSIYLPDCCDYAVVLAKYA 300
QY 549 YPLVHSYETVELYERKYDDPMFKHLVLAQVYRGAMVELANSIYLPDCCDYAVVLAKYA 608
DB 301 DKYINISMKHPQEKKTYSLSFSDSLFSAVKNFTELASFSERLDQFDSNPIILRMNDOL 360
QY 609 DKYISMKHPQEKKTYSLSFSDSLFSAVKNFTELASFSERLDQFDSNPIILRMNDOL 668
DB 361 MFLERAFIDPLGLPDRPFRHVIYAPSSHNKYAGESPFGIYDALFDIESKVDPSKAMGDV 420

Db 669 MFLERAFDIDGLDREFFRYVIVAPSSHNKYGESFPGIADLFJESKVDPSKAMGEV 728
OY 421 KROISVAFTVOAAEFTLSEVA 442
Db 729 KROIVAAFTVOAAEFTLSEVA 750

RESULT 5.

US-09-999-832A-618
Sequence 618, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OR INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 1998-04-27
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2%; Score 2288; DB 10; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSSAPPDSSWRSLKVSYNVGPFTGNFSTOKVKMHISTNEVTIRYINIGTLRGAVEP 60
DB 309 MGSSAPPDSSWRSLKVSYPYVNGPFTGNFSTOKVKMHISTNEVTIRYINIGTLRGAVEP 368

QY 61 DRYVILGGHRDSWVFGIDPQSGAAVYHETVRSFGLTKEGMRPRRTLLFASMDAEEFGL 120
DB 369 DRYVILGGHRDSWVFGIDPQSGAAVYHETVRSFGLTKEGMRPRRTLLFASMDAEEFGL 428
QY 121 LGSTEWADNSRLLOERGVATINADSSIEGVYTLRVDCPTPLMYSLVYNLTETELSPDEGF 180
DB 429 LGSTEWADNSRLLOERGVATINADSSIEGVYTLRVDCPTPLMYSLVYNLTETELSPDEGF 488
QY 181 ECKSLYESWTKKSPSPERSGMPRIKSLGSGNDPEYFQRLGIASGRARYTNWETNKFSG 240
DB 489 ECKSLYESWTKKSPSPERSGMPRIKSLGSGNDPEYFQRLGIASGRARYTNWETNKFSG 548
QY 241 YPLVHSVYETELVEKEFYDPMFKYHLFVAQYRGVWFELANSIVLPEDCRDYAVVLKRYA 300
DB 549 YPLVHSVYETELVEKEFYDPMFKYHLFVAQYRGVWFELANSIVLPEDCRDYAVVLKRYA 608
QY 301 DKIXNISMKHPQEMKTYSLSDSLFSAVKNTETLASKSEKLODFDKSNPILLRMNDOL 360
DB 609 DKIXNISMKHPQEMKTYSLSDSLFSAVKNTETLASKSEKLODFDKSNPILLRMNDOL 668
QY 361 MFLERAFIDPLGLPDRPPYRHYIYAPSSHNKYAGSPFGITDALFDIESKYDPSKMGDV 420
DB 669 MFLERAFIDPLGLPDRPPYRHYIYAPSSHNKYAGSPFGITDALFDIESKYDPSKMGDV 728
QY 421 KROIISAAFTVOAAETLSEVA 442
DB 729 KROIISAAFTVOAAETLSEVA 750

RESULT 6
US-09-895-793-944
Sequence 944, Application US/09895793
Publication No. US20020192763A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 944
LENGTH: 750
TYPE: PRT
ORGANISM: Homo sapiens

Query Match 98.2%; Score 2288; DB 10; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

PRIOR APPLICATION NUMBER: 60/081955
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081817
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 PRIOR APPLICATION NUMBER: 60/082569
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 PRIOR APPLICATION NUMBER: 60/082700
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 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796
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 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-13
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 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2%; Score 2288; DB 11; Length 750;
 Best Local Similarity 98.0%; Pred. No. 7.3e-217;
 Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

1 MGSAPPDSSWRGSLKVSYNVGPFTGNFSTQKVMHISTNEVTRIVNIGTLGAVEP 60
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 309 MGSAPPDSSWRGSLKVSYNVGPFTGNFSTQKVMHISTNEVTRIVNIGTLGAVEP 368
 |||||
 61 DRYVILGGRDQSWVFGGIDPOGAAVHEIVRSFCTLKEGMRPRRTILFASWDAEEFGL 120
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 369 DRYVILGGRDQSWVFGGIDPOGAAVHEIVRSFCTLKEGMRPRRTILFASWDAEEFGL 428
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 121 LGSTWAEADNSRFLDQFRVAYINADSSIEGNTYTLAVDCTPLMYSIVYULTELSKSPDGEF 180
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 429 LGSTWAEADNSRFLDQFRVAYINADSSIEGNTYTLAVDCTPLMYSIVYULTELSKSPDGEF 488
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 181 ESKSLYESWTGKSPSPERSGMPRIKSLGSGNDFEYFQRLGIASGRARYTKWETNKFSG 240
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 489 ESKSLYESWTGKSPSPERSGMPRIKSLGSGNDFEYFQRLGIASGRARYTKWETNKFSG 548
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 241 YPLYSVYETTELVEKFDPMFKYHLJVAQVRGAWFELANSIVLPFCRDYAAVLRKYA 300
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 549 YPLYSVYETTELVEKFDPMFKYHLJVAQVRGAWFELANSIVLPFCRDYAAVLRKYA 608
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 301 DKYINISMKHPQDMKTYSLSPDSLSAVNFTFELISKESERLODPDKSPYILRMANDOL 360
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 609 DKYINISMKHPQDMKTYSLSPDSLSAVNFTFELISKESERLODPDKSPYILRMANDOL 668
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 361 MFLERAFIDPLGDPDFRYHVIYAPSSHNKYAGESFPDIYDALDIESKVPDSKAMGV 420
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 421 KROISVAAEFTVOAAAEFTLSEVA 442
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 729 KROISVAAEFTVOAAAEFTLSEVA 750
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RESULT 8
 US-09-978-608A-618
 ; Sequence 618, Application US/09978608A
 ; Publication No. US20030045462A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashtkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey J.
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher

```

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978, 608A
; NUMBER OF SEQ ID NOS: 624
; PRIOR Application removed - See File Wrapper or Palm
; SEQ ID NO 618
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-978-608A-618

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Query Match          98.2%; Score 2288; DB 11; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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1 MGSAAPPSSWRSGLKVSINVGPGFTGNFSTQKVKMHISTNEVRIYVIGTLGAVEP 60
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309 MGSAAPPSSWRSGLKVSINVGPGFTGNFSTQKVKMHISTNEVRIYVIGTLGAVEP 368
61 DRYVILGHRDSWVGGLDPOSGAAVHETVRSFGTLKKEGRPRRTILFASWDAEEFGL 120
DRYVILGHRDSWVGGLDPOSGAAVHETVRSFGTLKKEGRPRRTILFASWDAEEFGL 428
121 LGSTMAEDNSRLQERGVAYINADSIIEGNTTLRVDCPTPLMYSLVYNLTKEKSPDEGF 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
429 LGSTMAEDNSRLQERGVAYINADSIIEGNTTLRVDCPTPLMYSLVYNLTKEKSPDEGF 488
181 EGKSLYESWTKKSPSPESGMPRIKSLGSGNDFEYFQRLGIASGRARTKMWETNKESG 240
EGKSLYESWTKKSPSPESGMPRIKSLGSGNDFEYFQRLGIASGRARTKMWETNKESG 548
241 YPLHSVYETELVEKFTDPMFKYHLTYAOVRGWVFEELANSIVLPDCRDYAVVLRKYA 300
YPLHSVYETELVEKFTDPMFKYHLTYAOVRGWVFEELANSIVLPDCRDYAVVLRKYA 608
301 DKYINISMKHPQEMKTYSLSPDSLFSAYKNFTEIASKFSERLQDDPKSNPILRRMNDOL 360
DKYINISMKHPQEMKTYSLSPDSLFSAYKNFTEIASKFSERLQDDPKSNPILRRMNDOL 668
609 DKYINISMKHPQEMKTYSLSPDSLFSAYKNFTEIASKFSERLQDDPKSNPILRRMNDOL 668
361 MFLERAFIDPLGLPRPFYRHYIYAPSSHNKAYAGSPFGIYDALDIESKVPDSKAWGV 420
MFLERAFIDPLGLPRPFYRHYIYAPSSHNKAYAGSPFGIYDALDIESKVPDSKAWGV 728
669 MFLERAFIDPLGLPRPFYRHYIYAPSSHNKAYAGSPFGIYDALDIESKVPDSKAWGV 728
421 KROIYVAAFTVOAAAEITLSEVA 442
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729 KROIYVAAFTVOAAAEITLSEVA 750

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RESULT 9
US-09-978-585A-618
; Sequence 618, Application US/0978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan

```

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; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978, 585A
; NUMBER OF SEQ ID NOS: 624
; PRIOR Application removed - See File Wrapper or Palm
; SEQ ID NO 618
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-978-585A-618

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Query Match          98.2%; Score 2288; DB 11; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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1 MGSAAPPSSWRSGLKVSINVGPGFTGNFSTQKVKMHISTNEVRIYVIGTLGAVEP 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
309 MGSAAPPSSWRSGLKVSINVGPGFTGNFSTQKVKMHISTNEVRIYVIGTLGAVEP 368
61 DRYVILGHRDSWVGGLDPOSGAAVHETVRSFGTLKKEGRPRRTILFASWDAEEFGL 120
DRYVILGHRDSWVGGLDPOSGAAVHETVRSFGTLKKEGRPRRTILFASWDAEEFGL 428
121 LGSTMAEDNSRLQERGVAYINADSIIEGNTTLRVDCPTPLMYSLVYNLTKEKSPDEGF 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
429 LGSTMAEDNSRLQERGVAYINADSIIEGNTTLRVDCPTPLMYSLVYNLTKEKSPDEGF 488
181 EGKSLYESWTKKSPSPESGMPRIKSLGSGNDFEYFQRLGIASGRARTKMWETNKESG 240
EGKSLYESWTKKSPSPESGMPRIKSLGSGNDFEYFQRLGIASGRARTKMWETNKESG 548
241 YPLHSVYETELVEKFTDPMFKYHLTYAOVRGWVFEELANSIVLPDCRDYAVVLRKYA 300
YPLHSVYETELVEKFTDPMFKYHLTYAOVRGWVFEELANSIVLPDCRDYAVVLRKYA 608
301 DKYINISMKHPQEMKTYSLSPDSLFSAYKNFTEIASKFSERLQDDPKSNPILRRMNDOL 360
DKYINISMKHPQEMKTYSLSPDSLFSAYKNFTEIASKFSERLQDDPKSNPILRRMNDOL 668
609 DKYINISMKHPQEMKTYSLSPDSLFSAYKNFTEIASKFSERLQDDPKSNPILRRMNDOL 668
361 MFLERAFIDPLGLPRPFYRHYIYAPSSHNKAYAGSPFGIYDALDIESKVPDSKAWGV 420
MFLERAFIDPLGLPRPFYRHYIYAPSSHNKAYAGSPFGIYDALDIESKVPDSKAWGV 728
669 MFLERAFIDPLGLPRPFYRHYIYAPSSHNKAYAGSPFGIYDALDIESKVPDSKAWGV 728
421 KROIYVAAFTVOAAAEITLSEVA 442
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
729 KROIYVAAFTVOAAAEITLSEVA 750

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RESULT 10

US-09-978-191A-618
 : Sequence 618, Application US/09978191A
 : Publication No. US20030050239A1
 : GENERAL INFORMATION:
 : APPLICANT: Ashkenazi, Avi
 : APPLICANT: Baker Kevin P.
 : APPLICANT: Botstein, David
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Eaton, Dan
 : APPLICANT: Ferrara, Napoleon
 : APPLICANT: Filvaroff, Ellen
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gao, Wei-Qiang
 : APPLICANT: Gerber, Hanspeter
 : APPLICANT: Gerritsen, Mary E.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Hillan, Kenneth J.
 : APPLICANT: Kijavitt, Ivar J.
 : APPLICANT: Kuo, Sophia S.
 : APPLICANT: Napier, Mary A.
 : APPLICANT: Pan, James;
 : APPLICANT: Paoni, Nicholas F.
 : APPLICANT: Roy, Margaret Ann
 : APPLICANT: Shelton, David L.
 : APPLICANT: Stewart, Timothy A.
 : APPLICANT: Tumas, Daniel
 : APPLICANT: Williams, P. Mickey
 : APPLICANT: Wood, William I.
 : TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
 : FILE OF INVENTION: Acids Encoding the Same
 : FILE REFERENCE: P2630P1C4
 : CURRENT APPLICATION NUMBER: US/09/978,191A
 : PRIOR FILING DATE: 2001-10-15
 : PRIOR APPLICATION NUMBER: 09/918585
 : PRIOR FILING DATE: 2001-07-30
 : PRIOR APPLICATION NUMBER: 60/062250
 : PRIOR FILING DATE: 1997-10-17
 : PRIOR APPLICATION NUMBER: 60/064249
 : PRIOR FILING DATE: 1997-11-03
 : PRIOR APPLICATION NUMBER: 60/065311
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 : PRIOR APPLICATION NUMBER: 60/066364
 : PRIOR FILING DATE: 1997-11-21
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 : PRIOR APPLICATION NUMBER: 60/077632
 : PRIOR FILING DATE: 1998-03-11
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 : PRIOR APPLICATION NUMBER: 60/078004
 : PRIOR FILING DATE: 1998-03-13
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 : PRIOR APPLICATION NUMBER: 60/078936
 : PRIOR FILING DATE: 1998-03-20
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 : PRIOR APPLICATION NUMBER: 60/079294
 : PRIOR FILING DATE: 1998-03-25
 : PRIOR APPLICATION NUMBER: 60/079656
 : PRIOR FILING DATE: 1998-03-26
 : PRIOR APPLICATION NUMBER: 60/079664
 : PRIOR FILING DATE: 1998-03-27
 : PRIOR APPLICATION NUMBER: 60/079689

: PRIOR FILING DATE: 1998-03-27
 : PRIOR APPLICATION NUMBER: 60/079663
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 : PRIOR APPLICATION NUMBER: 60/082704
 : PRIOR FILING DATE: 1998-04-22
 : PRIOR APPLICATION NUMBER: 60/082804
 : PRIOR FILING DATE: 1998-04-22
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 : PRIOR FILING DATE: 1998-04-22
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 : PRIOR APPLICATION NUMBER: 60/083392
 : PRIOR FILING DATE: 1998-04-29
 : PRIOR APPLICATION NUMBER: 60/083495
 : PRIOR FILING DATE: 1998-04-29
 : PRIOR APPLICATION NUMBER: 60/083496
 : PRIOR FILING DATE: 1998-04-29

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PRIORITY APPLICATION NUMBER: 60/083499
PRIORITY FILING DATE: 1998-04-29
PRIORITY APPLICATION NUMBER: 60/083545
PRIORITY FILING DATE: 1998-04-29
PRIORITY APPLICATION NUMBER: 60/083554
PRIORITY FILING DATE: 1998-04-29
PRIORITY APPLICATION NUMBER: 60/083558
PRIORITY FILING DATE: 1998-04-29
PRIORITY APPLICATION NUMBER: 60/083559
PRIORITY FILING DATE: 1998-04-29
PRIORITY APPLICATION NUMBER: 60/083500
PRIORITY FILING DATE: 1998-04-29
PRIORITY APPLICATION NUMBER: 60/083742
PRIORITY FILING DATE: 1998-04-30
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PRIORITY FILING DATE: 1998-05-07
PRIORITY APPLICATION NUMBER: 60/084600
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PRIORITY APPLICATION NUMBER: 60/084627
PRIORITY FILING DATE: 1998-05-07
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PRIORITY FILING DATE: 1998-05-07
PRIORITY APPLICATION NUMBER: 60/085339
PRIORITY FILING DATE: 1998-05-13
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PRIORITY FILING DATE: 1998-05-13
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PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085700
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085689
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085579
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085580
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085573
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085704
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: 60/085697

Query Match          98.2%; Score 2288; DB 11; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPRDSMGSGLKSTVNVGPGTGNFSTOKVKMHINHSNEDVRIYVIGTLRGAVP 60
    |||||||
DB 309 MGSAPRDSMGSGLKSTVNVGPGTGNFSTOKVKMHINHSNEDVRIYVIGTLRGAVP 368
    |||||||
QY 61 DRYVILGHRDQVNGGIDPQSGAAYVHEVTSFGTLKKGMRPRTILFASMDAEEPL 120
    |||||||
DB 369 DRYVILGHRDQVNGGIDPQSGAAYVHEVTSFGTLKKGMRPRTILFASMDAEEPL 428
    |||||||
QY 121 LGSTMAEDNSRLDERGVAYINADSLIEGNTLRVDTPLMYSLVYNLTKEKSPDEGF 180
    |||||||
DB 429 LGSTMAEDNSRLDERGVAYINADSLIEGNTLRVDTPLMYSLVYNLTKEKSPDEGF 488
    |||||||
QY 181 ECKSLYESWTKKSPSEFSGMPRISKLSGNDPEVFPORLGIASGRARYTKMETNKFSG 240
    |||||||
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DB 489 ECKSLYESWTKKSPSEFSGMPRISKLSGNDPEVFPORLGIASGRARYTKMETNKFSG 548
    |||||||
QY 241 YPLVHSVETVELVEKFPYDMFKYHLTVAVRGGMPELANSLVLPEDCDVAVVLKRYA 300
    |||||||
DB 549 YPLVHSVETVELVEKFPYDMFKYHLTVAVRGGMPELANSLVLPEDCDVAVVLKRYA 608
    |||||||
QY 301 DKTYNISMKHPQMKYSLSFDSLFSQVKNFTETASKFSERLQDPKSNPILRMNDOL 360
    |||||||
DB 609 DKTYNISMKHPQMKYSLSFDSLFSQVKNFTETASKFSERLQDPKSNPILRMNDOL 668
    |||||||
QY 361 MFLERAFIDPLGLDPRPFYRHVITYAPSSHNKYAGESPFGIYDALFDIESKVDPSKMGDV 420
    |||||||
DB 669 MFLERAFIDPLGLDPRPFYRHVITYAPSSHNKYAGESPFGIYDALFDIESKVDPSKMGDV 728
    |||||||
QY 421 KROIYVAALFTVQAAETLSVA 442
    |||||||
DB 729 KROIYVAALFTVQAAETLSVA 750
    |||||||

RESULT 11
US-09-978-403A-618
Sequence 618, Application US/09978403A
Publication No. US20030050240A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James:
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
PRIORITY FILING DATE: 2002-03-19
PRIORITY APPLICATION NUMBER: 09/918585
PRIORITY FILING DATE: 2001-07-30
PRIORITY APPLICATION NUMBER: 60/062250
PRIORITY FILING DATE: 1997-10-17
PRIORITY APPLICATION NUMBER: 60/064249
PRIORITY FILING DATE: 1997-11-03
PRIORITY APPLICATION NUMBER: 60/065311
PRIORITY FILING DATE: 1997-11-13
PRIORITY APPLICATION NUMBER: 60/066364
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PRIORITY APPLICATION NUMBER: 60/077450
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PRIORITY FILING DATE: 1998-03-11
PRIORITY APPLICATION NUMBER: 60/077641
PRIORITY FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/077649	PRIOR FILING DATE: 1998-03-11	PRIOR APPLICATION NUMBER: 60/077791	PRIOR FILING DATE: 1998-03-12	PRIOR APPLICATION NUMBER: 60/078004	PRIOR FILING DATE: 1998-03-13	PRIOR APPLICATION NUMBER: 60/078886	PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/078936	PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/078910	PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/078939	PRIOR FILING DATE: 1998-03-20	PRIOR APPLICATION NUMBER: 60/079294	PRIOR FILING DATE: 1998-03-25	PRIOR APPLICATION NUMBER: 60/079656	PRIOR FILING DATE: 1998-03-26	PRIOR APPLICATION NUMBER: 60/079664	PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/079689	PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/079663	PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/079728	PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/079786	PRIOR FILING DATE: 1998-03-27	PRIOR APPLICATION NUMBER: 60/079920	PRIOR FILING DATE: 1998-03-30	PRIOR APPLICATION NUMBER: 60/079923	PRIOR FILING DATE: 1998-03-30	PRIOR APPLICATION NUMBER: 60/080105	PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080107	PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080165	PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080194	PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080327	PRIOR FILING DATE: 1998-04-01	PRIOR APPLICATION NUMBER: 60/080328	PRIOR FILING DATE: 1998-04-01	PRIOR APPLICATION NUMBER: 60/080333	PRIOR FILING DATE: 1998-04-01	PRIOR APPLICATION NUMBER: 60/080334	PRIOR FILING DATE: 1998-04-01	PRIOR APPLICATION NUMBER: 60/081070	PRIOR FILING DATE: 1998-04-08	PRIOR APPLICATION NUMBER: 60/081049	PRIOR FILING DATE: 1998-04-08	PRIOR APPLICATION NUMBER: 60/081071	PRIOR FILING DATE: 1998-04-08	PRIOR APPLICATION NUMBER: 60/081195	PRIOR FILING DATE: 1998-04-08	PRIOR APPLICATION NUMBER: 60/081203	PRIOR FILING DATE: 1998-04-09	PRIOR APPLICATION NUMBER: 60/081229	PRIOR FILING DATE: 1998-04-09	PRIOR APPLICATION NUMBER: 60/081555	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081819	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081952	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081838	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/082568	PRIOR FILING DATE: 1998-04-21	PRIOR APPLICATION NUMBER: 60/082565
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1	PRIOR FILING DATE: 1998-04-21	
2	PRIOR APPLICATION NUMBER: 60/082704	
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4	PRIOR APPLICATION NUMBER: 60/082804	
5	PRIOR FILING DATE: 1998-04-22	
6	PRIOR APPLICATION NUMBER: 60/082700	
7	PRIOR FILING DATE: 1998-04-22	
8	PRIOR APPLICATION NUMBER: 60/082797	
9	PRIOR FILING DATE: 1998-04-22	
10	PRIOR APPLICATION NUMBER: 60/082796	
11	PRIOR FILING DATE: 1998-04-23	
12	PRIOR APPLICATION NUMBER: 60/083336	
13	PRIOR FILING DATE: 1998-04-27	
14	PRIOR APPLICATION NUMBER: 60/083322	
15	PRIOR FILING DATE: 1998-04-28	
16	PRIOR APPLICATION NUMBER: 60/083392	
17	PRIOR FILING DATE: 1998-04-29	
18	PRIOR APPLICATION NUMBER: 60/083495	
19	PRIOR FILING DATE: 1998-04-29	
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21	PRIOR FILING DATE: 1998-04-29	
22	PRIOR APPLICATION NUMBER: 60/083499	
23	PRIOR FILING DATE: 1998-04-29	
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35	PRIOR FILING DATE: 1998-04-30	
36	PRIOR APPLICATION NUMBER: 60/084366	
37	PRIOR FILING DATE: 1998-05-05	
38	PRIOR APPLICATION NUMBER: 60/084414	
39	PRIOR FILING DATE: 1998-05-06	
40	PRIOR APPLICATION NUMBER: 60/084441	
41	PRIOR FILING DATE: 1998-05-06	
42	PRIOR APPLICATION NUMBER: 60/084637	
43	PRIOR FILING DATE: 1998-05-07	
44	PRIOR APPLICATION NUMBER: 60/084639	
45	PRIOR FILING DATE: 1998-05-07	
46	PRIOR APPLICATION NUMBER: 60/084640	
47	PRIOR FILING DATE: 1998-05-07	
48	PRIOR APPLICATION NUMBER: 60/084598	
49	PRIOR FILING DATE: 1998-05-07	
50	PRIOR APPLICATION NUMBER: 60/084600	
51	PRIOR FILING DATE: 1998-05-07	
52	PRIOR APPLICATION NUMBER: 60/084627	
53	PRIOR FILING DATE: 1998-05-07	
54	PRIOR APPLICATION NUMBER: 60/084643	
55	PRIOR FILING DATE: 1998-05-07	
56	PRIOR APPLICATION NUMBER: 60/085339	
57	PRIOR FILING DATE: 1998-05-13	
58	PRIOR APPLICATION NUMBER: 60/085338	
59	PRIOR FILING DATE: 1998-05-13	
60	PRIOR APPLICATION NUMBER: 60/085323	
61	PRIOR FILING DATE: 1998-05-13	
62	PRIOR APPLICATION NUMBER: 60/085582	
63	PRIOR FILING DATE: 1998-05-15	
64	PRIOR APPLICATION NUMBER: 60/085700	
65	PRIOR FILING DATE: 1998-05-15	
66	PRIOR APPLICATION NUMBER: 60/085699	
67	PRIOR FILING DATE: 1998-05-15	
68	PRIOR APPLICATION NUMBER: 60/085579	
69	PRIOR FILING DATE: 1998-05-15	
70	PRIOR APPLICATION NUMBER: 60/085580	
71	PRIOR FILING DATE: 1998-05-15	
72	PRIOR APPLICATION NUMBER: 60/085573	
73	PRIOR FILING DATE: 1998-05-15	

PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2%; Score 2288; DB 11; Length 750;
 Best Local Similarity 98.0%; Pred. No. 7.3e-217;
 Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAAPPSSWNGSLKVSYNVGPFTGNFSTQKVMHHSSTNEVRIYNVIGTLGAVEP 60
 DB 309 MGSAAPPSSWNGSLKVSYNVGPFTGNFSTQKVMHHSSTNEVRIYNVIGTLGAVEP 368
 QY 61 DRYVILGHRDSWVVGIDIPGSAVVEHYVASFCTLKEGMRPRRTILFASWDAEEFGL 120
 DB 369 DRYVILGHRDSWVVGIDIPGSAVVEHYVASFCTLKEGMRPRRTILFASWDAEEFGL 428
 QY 121 LGSTMAEDNSHLOERGVAYINADSSIEGNTLAVDCTPLMTSLVYNLTKEKSPDEGF 180
 DB 429 LGSTMAEDNSHLOERGVAYINADSSIEGNTLAVDCTPLMTSLVYNLTKEKSPDEGF 488
 QY 181 EGSLSYEEMTKKSPSPERSGMPRIKSLGSGNDFEYFQRLGIASGRARTKMTNKFSG 240
 DB 489 EGSLSYEEMTKKSPSPERSGMPRIKSLGSGNDFEYFQRLGIASGRARTKMTNKFSG 548
 QY 241 YPLXSHVYETELVEKFFYDPMKHYLTVAOYVGNVFEIANSIVLPDCRDYAVVLRKYA 300
 DB 549 YPLXSHVYETELVEKFFYDPMKHYLTVAOYVGNVFEIANSIVLPDCRDYAVVLRKYA 608
 QY 301 DKIVYSKHHQEMKTYSLSPDSLFSAVKNFTLEISKSSERLODFDKSNPILRRMNDOL 360
 DB 609 DKIVYSKHHQEMKTYSLSPDSLFSAVKNFTLEISKSSERLODFDKSNPILRRMNDOL 668
 QY 361 MFLERAFIDPLGIPRPYRHVITAPSSHNKYGSPFGIYDALDISKVPKAMGVY 420
 DB 669 MFLERAFIDPLGIPRPYRHVITAPSSHNKYGSPFGIYDALDISKVPKAMGVY 728
 QY 421 KRQISVAFTVOAAETLSEVA 442
 DB 729 KRQIVAAFTVOAAETLSEVA 750

RESULT 12
 US-09-978-564A-618
 Sequence 618, Application US/09978564A
 Publication No. US20030050241A1
 GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerltsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC25
 CURRENT APPLICATION NUMBER: 2001-10-16
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2%; Score 2288; DB 11; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPPDSSWRGSLKSYNVPFGFTGNFSTQKKMHITHSTNETRYNYIGTLRGAVEP 60
DB MGSAPPDSSWRGSLKPYNNPGFTGNFSTQKKMHITHSTNETRYNYIGTLRGAVEP 368
QY 61 DRYVILGHRDSWYFVGIDPOSGAAVYHEVYRSPGTLKKEGMRPRRTILFASMPDAEEFGL 120
DB DRYVILGHRDSWYFVGIDPOSGAAVYHEVYRSPGTLKKEGMRPRRTILFASMPDAEEFGL 428
QY 121 LGSTWMAEDNSRLQERGVAVYINDSSIEGNYTLRVDCPTPLMSLVYNTLKEKSPDEGF 180
DB LGSTWMAEDNSRLQERGVAVYINDSSIEGNYTLRVDCPTPLMSLVYNTLKEKSPDEGF 488
QY 429 LGSTWMAEDNSRLQERGVAVYINDSSIEGNYTLRVDCPTPLMSLVYNTLKEKSPDEGF 488
DB LGSTWMAEDNSRLQERGVAVYINDSSIEGNYTLRVDCPTPLMSLVYNTLKEKSPDEGF 488
QY 181 EGSLSYSWTKKSSPSPSGMFRISKLGSNDPEVFFQRLGIASGRARYTKMNTKNSFG 240
DB EGSLSYSWTKKSSPSPSGMFRISKLGSNDPEVFFQRLGIASGRARYTKMNTKNSFG 548
QY 489 EGSLSYSWTKKSSPSPSGMFRISKLGSNDPEVFFQRLGIASGRARYTKMNTKNSFG 548
DB EGSLSYSWTKKSSPSPSGMFRISKLGSNDPEVFFQRLGIASGRARYTKMNTKNSFG 548
QY 241 YPLXHSYETEYELVEKYDDPMFKYHLTVAGYRGSMVELANSIYLPDPCRDYAVVLRKYA 300
DB YPLXHSYETEYELVEKYDDPMFKYHLTVAGYRGSMVELANSIYLPDPCRDYAVVLRKYA 608
QY 549 YPLXHSYETEYELVEKYDDPMFKYHLTVAGYRGSMVELANSIYLPDPCRDYAVVLRKYA 608
DB YPLXHSYETEYELVEKYDDPMFKYHLTVAGYRGSMVELANSIYLPDPCRDYAVVLRKYA 608
QY 301 DKYINISMKHPQEMKITYSLSPDSLFSVKNFTELTASKFSERLQDFDKSNPILLRMNDOL 360
DB DKYINISMKHPQEMKITYSLSPDSLFSVKNFTELTASKFSERLQDFDKSNPILLRMNDOL 668
QY 609 DKYISIMKHQEMKITYSVSPDSLFSVKNFTELTASKFSERLQDFDKSNPILLRMNDOL 668
DB DKYISIMKHQEMKITYSVSPDSLFSVKNFTELTASKFSERLQDFDKSNPILLRMNDOL 668
QY 361 MFLERATIDPLGLPDRPFYRHYVYIAPSSHNKYAGESPFGIYDALFDIESKYVDPKANGDV 420
DB MFLERATIDPLGLPDRPFYRHYVYIAPSSHNKYAGESPFGIYDALFDIESKYVDPKANGDV 728
QY 669 MFLERATIDPLGLPDRPFYRHYVYIAPSSHNKYAGESPFGIYDALFDIESKYVDPKANGDV 728
DB MFLERATIDPLGLPDRPFYRHYVYIAPSSHNKYAGESPFGIYDALFDIESKYVDPKANGDV 728
QY 421 KROISVAAFYVOAAETLSEYA 442
DB KROISVAAFYVOAAETLSEYA 750
QY 729 KROLYVAATYVOAAETLSEYA 750
DB KROLYVAATYVOAAETLSEYA 750

RESULT 13
US-09-999-833A-618
Sequence 618, Application US/0999833A
Publication No. US20030054405A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Olang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.2%; Score 2288; DB 11; Length 750;
Best Local Similarity 98.0%; Pred. No. 7.3e-217;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

1 MGSAPPDSSWMSGLKVSYNVNGPGFTGNFSTOKYKMHISTNEVTRIVNIGTLGAVEP 60
|||||
309 MGSAPPDSSWMSGLKVPYVNGPGFTGNFSTOKYKMHISTNEVTRIVNIGTLGAVEP 368
61 DRYVLGGHRSWVGGLDPOSGAAVVEHYRSFETLKEGRRPRTILFASWDAEEGL 120
|||||
369 DRYVLGGHRSWVGGLDPOSGAAVVEHYRSFETLKEGRRPRTILFASWDAEEGL 428
121 LGSTFMAEDNSRLQERGVAYINADSSIEGNTLVDCSTPLMYSIVYULFTELKSPDGEF 180
|||||
429 LGSTFMAEDNSRLQERGVAYINADSSIEGNTLVDCSTPLMYSIVYULFTELKSPDGEF 488
181 ECKSLYESMTKSPSPERSGMPRTSKLGSNDFEVFPORLGIASGRARYTNMETNKEGSG 240
489 ECKSLYESMTKSPSPERSGMPRTSKLGSNDFEVFPORLGIASGRARYTNMETNKEGSG 548
241 YPLHSYVETELVEKFTDPMFKYTLTYAQVRGCVFELANSIVLPCCRDYAAVLRKYA 300
549 YPLHSYVETELVEKFTDPMFKYTLTYAQVRGCVFELANSIVLPCCRDYAAVLRKYA 608
301 DKYVNSKHPQEMKTYSLFSDSLFSAYKNFTETLASKRSERLQDDKSNPILIRMMNOL 360
609 DKYVNSKHPQEMKTYSLFSDSLFSAYKNFTETLASKRSERLQDDKSNPILIRMMNOL 668

361 MFLERAFIDPLGDPDPYRHYVYAPSSHNKYAGSEFFGIYDALFDIESKYDPSKMGDV 420
|||||
669 MFLERAFIDPLGDPDPYRHYVYAPSSHNKYAGSEFFGIYDALFDIESKYDPSKMGDV 728
421 KRQISVAAPFYQAAAEITLSEVA 442
729 KRQIYVAAPFYQAAAEITLSEVA 750
RESULT 14
US-09-981-915A-618
; Sequence 618, Application US/09981915A
; General Information: US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C12
; CURRENT APPLICATION NUMBER: US/09/981,915A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1997-11-21
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; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20

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 : Sequence 618, Application US/09978824
 : Publication No. US20030055216a1
 : GENERAL INFORMATION:
 : APPLICANT: Ashkenazi, Avi
 : APPLICANT: Baker Kevin P.
 : APPLICANT: Bolstein, David
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Eaton, Dan
 : APPLICANT: Ferrara, Napoleon
 : APPLICANT: Filvaroff, Ellen
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gao, Wei-Qiang
 : APPLICANT: Gerber, Hanspeter
 : APPLICANT: Gerlisen, Mary E.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Hillan, Kenneth J.
 : APPLICANT: Kljavin, Ivar J.
 : APPLICANT: Kuo, Sophia S.
 : APPLICANT: Napier, Mary A.
 : APPLICANT: Pan, James;
 : APPLICANT: Paoni, Nicholas F.
 : APPLICANT: Roy, Margaret Ann
 : APPLICANT: Shelton, David L.
 : APPLICANT: Stewart, Timothy A.
 : APPLICANT: Tumas, Daniel
 : APPLICANT: Williams, P. Mickey
 : APPLICANT: Wood, William I.
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 : FILE REFERENCE: P2630P1C14
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 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 98.28; Score 2288; DB 11; Length 750;
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 DB 369 DRYVILGHRDWMYFGSIDPQSGAAVYHETVRSFGLTKKGWRPRTILFASMDAEFGL 428
 QY 121 LGSTENAEADNSRLIOERGVAIYINADSSIEGNYTLRVDCPTLMVSLVHNLTKELSPDEGF 180
 DB 429 LGSTENAEADNSRLIOERGVAIYINADSSIEGNYTLRVDCPTLMVSLVHNLTKELSPDEGF 488
 QY 181 EGKSLYSEWTKKSPSPFSGMPRTSKLGSNDPEVFQORGLIASGRARYTKNETNFSG 240
 DB 489 EGKSLYSEWTKKSPSPFSGMPRTSKLGSNDPEVFQORGLIASGRARYTKNETNFSG 548
 QY 241 YPLYHSYETVELVEKEFYDPMFKYHLTVAOVRGMVELANSIYLPDCHDYAVVLKRYA 300
 DB 549 YPLYHSYETVELVEKEFYDPMFKYHLTVAOVRGMVELANSIYLPDCHDYAVVLKRYA 608
 QY 301 DKTYNISMKHPQEKITYSLFSDSLFSAVKNFTELAKFSERLQDFDKSNITLBMANDOL 360
 DB 609 DKTYNISMKHPQEKITYSLFSDSLFSAVKNFTELAKFSERLQDFDKSNITLBMANDOL 668
 QY 361 MFLERAFIDPLGLPDRFERYHVITYAPSSHKKYAGESPGLYDLDFDIESKVDPSKANGDV 420
 DB 669 MFLERAFIDPLGLPDRFERYHVITYAPSSHKKYAGESPGLYDLDFDIESKVDPSKANGDV 728
 QY 421 KRQISVAFTVQAAAEITLSEVA 442
 DB 729 KRQISVAFTVQAAAEITLSEVA 750

Search completed: October 4, 2003, 23:27:56
 Job time : 60 secs

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OM protein - protein search, using sw model

Run on: October 4, 2003, 23:20:12 ; Search time 35 Seconds
(without alignments)
534.326 Million cell updates/sec

Title: US-09-973-382C-2

Perfect score: 2329
Sequence: 1 MGSAPPDSSWRGSLKYSYN.....QISVAFTVOAAETLSEVA 442

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

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6: /cgn2_6/ptodata/2/1aa/Backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
	1	2288	98.2	707	1 US-08-528-122-18	Sequence 18, Appl
	2	2288	98.2	707	5 PCT-US95-11720-18	Sequence 18, Appl
	3	2288	98.2	750	1 US-08-325-553-2	Sequence 2, Appl
	4	2288	98.2	750	2 US-08-394-152A-2	Sequence 2, Appl
	5	2288	98.2	750	3 US-09-044-668-2	Sequence 2, Appl
	6	2288	98.2	750	4 US-08-705-477E-2	Sequence 2, Appl
	7	2281	97.9	693	4 US-08-705-477E-101	Sequence 101, App
	8	445.5	19.1	622	1 US-08-547-197-1	Sequence 1, Appl
	9	445.5	19.1	622	3 US-08-957-940-1	Sequence 1, Appl
	10	425	18.2	760	1 US-08-547-197-2	Sequence 2, Appl
	11	425	18.2	760	3 US-08-957-940-2	Sequence 2, Appl
	12	133.5	5.7	496	4 US-09-079-955-2	Sequence 2, Appl
	13	131.5	5.6	481	3 US-09-330-095-1	Sequence 1, Appl
	14	122.5	5.3	473	4 US-09-482-273-120	Sequence 120, App
	15	121.5	5.2	584	4 US-09-252-991A-18292	Sequence 18292, A
	16	119	5.1	718	4 US-09-252-991A-27540	Sequence 27540, A
	17	111	4.8	537	4 US-09-079-955-5	Sequence 5, Appl
	18	107.5	4.6	1447	4 US-09-376-330-17	Sequence 17, Appl
	19	103	4.4	873	4 US-09-252-991A-30504	Sequence 30504, A
	20	100.5	4.3	613	3 US-09-446-504-5	Sequence 5, Appl
	21	100.5	4.3	613	4 US-09-712-266-5	Sequence 5, Appl
	22	100.5	4.3	613	4 US-09-091-889A-2	Sequence 2, Appl
	23	100	4.3	19	1 US-08-325-553-11	Sequence 11, Appl
	24	100	4.3	19	2 US-08-394-152A-11	Sequence 11, Appl
	25	100	4.3	19	4 US-08-705-477E-11	Sequence 11, Appl
	26	97.5	4.2	414	4 US-09-634-238-271	Sequence 271, App
	27	96.5	4.1	377	2 US-08-929-922B-2	Sequence 2, Appl

28	96.5	4.1	377	3 US-09-342-394-2	Sequence 2, Appl
29	96.5	4.1	377	3 US-09-580-064-2	Sequence 2, Appl
30	96.5	4.1	377	3 US-09-011-540-2	Sequence 2, Appl
31	96.5	4.1	377	4 US-09-718-709-2	Sequence 2, Appl
32	96	4.1	396	3 US-09-082-310-2	Sequence 2, Appl
33	96	4.1	396	4 US-09-575-205-2	Sequence 2, Appl
34	95.5	4.1	597	4 US-09-252-991A-32073	Sequence 32073, A
35	95.5	4.1	981	2 US-08-649-046-2	Sequence 2, Appl
36	94.5	4.1	328	4 US-09-134-001C-3229	Sequence 3229, Ap
37	94.5	4.1	354	4 US-09-107-532A-5179	Sequence 5179, Ap
38	94.5	4.1	956	4 US-09-107-532A-5007	Sequence 5007, Ap
39	94	4.0	727	4 US-09-134-001C-4067	Sequence 4067, Ap
40	93.5	4.0	2233	2 US-08-569-853-1	Sequence 1, Appl
41	93.5	4.0	2233	3 US-08-569-853-2	Sequence 2, Appl
42	93.5	4.0	2233	3 US-08-987-439-1	Sequence 1, Appl
43	91.5	3.9	1151	4 US-09-134-001C-3242	Sequence 3242, Ap
44	91	3.9	514	2 US-08-865-311-2	Sequence 2, Appl
45	91	3.9	514	4 US-09-315-720-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-528-122-18
Sequence 18, Application US/08528122
Patent No. 5726044
GENERAL INFORMATION:
APPLICANT: LO, KIN-MING
APPLICANT: SUDO, YUKIO
APPLICANT: GILLIES, STEPHEN D.
TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/528,122
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: FIP-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 707 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..707
OTHER INFORMATION: /note= "EXTRACELLULAR DOMAIN OF
OTHER INFORMATION: PSMA"
US-08-528-122-18
Query Match 98.2%; Score 2288; DB 1; Length 707;

Best Local Similarity 98.0%; Pred. No. 1.6e-214;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPPDSSMRGSLKVSYNVGPFGTGNSTOKVKKHHISTNEVTIRIYNVIGTLGAVP 60
 DB 266 MGSAPPDSSMRGSLKVPYVNGPFGTGNSTOKVKKHHISTNEVTIRIYNVIGTLGAVP 325
 QY 61 DRYVILGHRDMSWVEFGIDPQSGAAVYHETVNSFGTLKKEGMRPRTILFASWDAEEFGL 120
 DB 326 DRYVILGHRDMSWVEFGIDPQSGAAVYHETVNSFGTLKKEGMRPRTILFASWDAEEFGL 385
 QY 121 LGSTEWAEDNSRLQDRGVAIYNADSSIGNTLRVDCIPLMYSLVYNTLTKELSPDEGF 180
 DB 386 LGSTEWAEDNSRLQDRGVAIYNADSSIGNTLRVDCIPLMYSLVYNTLTKELSPDEGF 445
 QY 181 EGSLSYESTWTKKSPSEFGMPRIKSLGSGNDFEYFQRLGIASGRARYTKMETKKEFSG 240
 DB 446 EGSLSYESTWTKKSPSEFGMPRIKSLGSGNDFEYFQRLGIASGRARYTKMETKKEFSG 505
 QY 241 YPLVHSVYETVELVEKFPDPMFKYHLTVAVRGWVFELANSIVLPDCRDYAVVLRKYA 300
 DB 506 YPLVHSVYETVELVEKFPDPMFKYHLTVAVRGWVFELANSIVLPDCRDYAVVLRKYA 565
 QY 301 DKYVNSMKHPQEMKTYSLSPDSLFSAVKNTFELASKFSERLQDPKSNPIYLRMMNDQL 360
 DB 566 DKYVNSMKHPQEMKTYSLSPDSLFSAVKNTFELASKFSERLQDPKSNPIYLRMMNDQL 625
 QY 361 MFLERAFIDPLGIDPRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVPDSKMGV 420
 DB 626 MFLERAFIDPLGIDPRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVPDSKMGV 685
 QY 421 KROIYAFTVOAAETLSEVA 442
 DB 686 KROIYAFTVOAAETLSEVA 707

RESULT 2

PCT-US95-11720-18
 ; Sequence 18, Application PC/TUS9511720
 ; GENERAL INFORMATION:

APPLICANT:
 TITLE OF INVENTION: EXPRESSION AND EXPORT TECHNOLOGY OF
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
 STREET: 125 HIGH STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/11720
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: PITCHER, EDMUND R.
 REGISTRATION NUMBER: 27,829
 REFERENCE/DOCKET NUMBER: FIP-001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-248-7000
 TELEFAX: 617-248-7100
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 707 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..707
 OTHER INFORMATION: /note="EXTRACELLULAR DOMAIN OF
 PSMA"
 PCT-US95-11720-18

Query Match 98.2%; Score 2288; DB 5; Length 707;
 Best Local Similarity 98.0%; Pred. No. 1.6e-214;
 Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGSAPPDSSMRGSLKVSYNVGPFGTGNSTOKVKKHHISTNEVTIRIYNVIGTLGAVP 60
 DB 266 MGSAPPDSSMRGSLKVPYVNGPFGTGNSTOKVKKHHISTNEVTIRIYNVIGTLGAVP 325
 QY 61 DRYVILGHRDMSWVEFGIDPQSGAAVYHETVNSFGTLKKEGMRPRTILFASWDAEEFGL 120
 DB 326 DRYVILGHRDMSWVEFGIDPQSGAAVYHETVNSFGTLKKEGMRPRTILFASWDAEEFGL 385
 QY 121 LGSTEWAEDNSRLQDRGVAIYNADSSIGNTLRVDCIPLMYSLVYNTLTKELSPDEGF 180
 DB 386 LGSTEWAEDNSRLQDRGVAIYNADSSIGNTLRVDCIPLMYSLVYNTLTKELSPDEGF 445
 QY 181 EGSLSYESTWTKKSPSEFGMPRIKSLGSGNDFEYFQRLGIASGRARYTKMETKKEFSG 240
 DB 446 EGSLSYESTWTKKSPSEFGMPRIKSLGSGNDFEYFQRLGIASGRARYTKMETKKEFSG 505
 QY 241 YPLVHSVYETVELVEKFPDPMFKYHLTVAVRGWVFELANSIVLPDCRDYAVVLRKYA 300
 DB 506 YPLVHSVYETVELVEKFPDPMFKYHLTVAVRGWVFELANSIVLPDCRDYAVVLRKYA 565
 QY 301 DKYVNSMKHPQEMKTYSLSPDSLFSAVKNTFELASKFSERLQDPKSNPIYLRMMNDQL 360
 DB 566 DKYVNSMKHPQEMKTYSLSPDSLFSAVKNTFELASKFSERLQDPKSNPIYLRMMNDQL 625
 QY 361 MFLERAFIDPLGIDPRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVPDSKMGV 420
 DB 626 MFLERAFIDPLGIDPRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVPDSKMGV 685
 QY 421 KROIYAFTVOAAETLSEVA 442
 DB 686 KROIYAFTVOAAETLSEVA 707

RESULT 3

US-08-325-553-2
 ; Sequence 2, Application US/08325553
 ; Patent No. 5538866
 ; GENERAL INFORMATION:

APPLICANT: Israeli, Ron S.
 APPLICANT: Heston, Warren D.W.
 TITLE OF INVENTION: THE PROSTATE-SPECIFIC MEMBRANE ANTIGEN
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/325,553
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

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: APPLICATION NUMBER: US/07/973.337A
: FILING DATE: 05 NOV 1992
: ATTORNEY/AGENT INFORMATION:
:   NAME: White, John P.
:   REGISTRATION NUMBER: 28,678
:   REFERENCE/DOCKET NUMBER: 1747/41426
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: (212) 977-9550
:     TELEFAX: (212) 664-0525
:     TELEX: 422523 COOP UI
:   INFORMATION FOR SEQ ID NO: 2:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 750 amino acids
:       TYPE: amino acid
:       TOPOLOGY: linear
:   MOLECULE TYPE: protein
: US-08-325-553-2

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Query Match      98.2%; Score 2288; DB 1; Length 750;
Best Local Similarity 98.0%; Pred. No. 1.8e-214;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MGSAAPPDSSWRGSLKAVYVNGPFTGNFSTOKYKMHISTNEYTRYNYIGTLKGAVER 60
   |||
DB 309 MGSAAPPDSSWRGSLKAVYVNGPFTGNFSTOKYKMHISTNEYTRYNYIGTLKGAVER 368
   |||
QY 61 DRVYILGCHDMSWVFGGIDPQSGAAYVHETVRSFGTLKKGWPRRTILFASMDAEFGL 120
   |||
DB 369 DRVYILGCHDMSWVFGGIDPQSGAAYVHETVRSFGTLKKGWPRRTILFASMDAEFGL 428
   |||
QY 121 LGSTEWAEADNSRLLOERGVAVINADSSIEGNYTLRVDCPTPLMYSLVNLTRELKSPDEGF 180
   |||
DB 429 LGSTEWAEADNSRLLOERGVAVINADSSIEGNYTLRVDCPTPLMYSLVNLTRELKSPDEGF 488
   |||
QY 181 EGSISLVSMTKSKSPSPFSGMPRIKSLGSGNDEVEFFQRIASGRARYTKNMTNFKFSG 240
   |||
DB 489 EGSISLVSMTKSKSPSPFSGMPRIKSLGSGNDEVEFFQRIASGRARYTKNMTNFKFSG 548
   |||
QY 241 YPLHSYETVELVEKEDYDMFKYHLTVAVOVRGMVPELANSIYLPDCRDYAVVLRKYA 300
   |||
DB 549 YPLHSYETVELVEKEDYDMFKYHLTVAVOVRGMVPELANSIYLPDCRDYAVVLRKYA 608
   |||
QY 301 DKTYINSMKHPQEKMTYSLSFDSLFSAVKNFTETIASKFSERLQDFKSNPILLRMNDQL 360
   |||
DB 609 DKTYINSMKHPQEKMTYSLSFDSLFSAVKNFTETIASKFSERLQDFKSNPILLRMNDQL 668
   |||
QY 361 MFLERAFIDPLGDPDRFFYRHVITYAPSSHNKYAGESPFGIYDALFDIESKVDPSKANGDY 420
   |||
DB 669 MFLERAFIDPLGDPDRFFYRHVITYAPSSHNKYAGESPFGIYDALFDIESKVDPSKANGDY 728
   |||
QY 421 KROIISVAFTVOAAAEITLSEVA 442
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DB 729 KROIISVAFTVOAAAEITLSEVA 750

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RESULT 4
US-08-394-152A-2
: Sequence 2, Application US/08394152A
: Patent No. 5935818
: GENERAL INFORMATION:
:   APPLICANT: Israel, Ron S.
:   APPLICANT: Heston, Warren D.W.
:   APPLICANT: Falt, William R.
:   TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
:   TITLE OF INVENTION: USES THEREOF
:   NUMBER OF SEQUENCES: 48
:   CORRESPONDENCE ADDRESS:
:     ADDRESSEE: Cooper & Dunham LLP
:     STREET: 1185 Avenue of the Americas
:     CITY: New York
:     STATE: New York
:     COUNTRY: United States of America
:     ZIP: 10036

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: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM 330 466 DX2
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/394.152A
:   FILING DATE: 24-FEB-95
:   CLASSIFICATION: 435
:   ATTORNEY/AGENT INFORMATION:
:     NAME: White, John P.
:     REGISTRATION NUMBER: 28,678
:     REFERENCE/DOCKET NUMBER: 41426-B
:     TELECOMMUNICATION INFORMATION:
:       TELEPHONE: (212) 278-0400
:       TELEFAX: (212) 391-0525
:     INFORMATION FOR SEQ ID NO: 2:
:       SEQUENCE CHARACTERISTICS:
:         LENGTH: 750 amino acids
:         TYPE: amino acid
:         TOPOLOGY: linear
:     MOLECULE TYPE: protein
: US-08-394-152A-2

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Query Match      98.2%; Score 2288; DB 2; Length 750;
Best Local Similarity 98.0%; Pred. No. 1.8e-214;
Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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   |||
DB 309 MGSAAPPDSSWRGSLKAVYVNGPFTGNFSTOKYKMHISTNEYTRYNYIGTLKGAVER 368
   |||
QY 61 DRVYILGCHDMSWVFGGIDPQSGAAYVHETVRSFGTLKKGWPRRTILFASMDAEFGL 120
   |||
DB 369 DRVYILGCHDMSWVFGGIDPQSGAAYVHETVRSFGTLKKGWPRRTILFASMDAEFGL 428
   |||
QY 121 LGSTEWAEADNSRLLOERGVAVINADSSIEGNYTLRVDCPTPLMYSLVNLTRELKSPDEGF 180
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DB 429 LGSTEWAEADNSRLLOERGVAVINADSSIEGNYTLRVDCPTPLMYSLVNLTRELKSPDEGF 488
   |||
QY 181 EGSISLVSMTKSKSPSPFSGMPRIKSLGSGNDEVEFFQRIASGRARYTKNMTNFKFSG 240
   |||
DB 489 EGSISLVSMTKSKSPSPFSGMPRIKSLGSGNDEVEFFQRIASGRARYTKNMTNFKFSG 548
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QY 241 YPLHSYETVELVEKEDYDMFKYHLTVAVOVRGMVPELANSIYLPDCRDYAVVLRKYA 300
   |||
DB 549 YPLHSYETVELVEKEDYDMFKYHLTVAVOVRGMVPELANSIYLPDCRDYAVVLRKYA 608
   |||
QY 301 DKTYINSMKHPQEKMTYSLSFDSLFSAVKNFTETIASKFSERLQDFKSNPILLRMNDQL 360
   |||
DB 609 DKTYINSMKHPQEKMTYSLSFDSLFSAVKNFTETIASKFSERLQDFKSNPILLRMNDQL 668
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   |||
DB 669 MFLERAFIDPLGDPDRFFYRHVITYAPSSHNKYAGESPFGIYDALFDIESKVDPSKANGDY 728
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QY 421 KROIISVAFTVOAAAEITLSEVA 442
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DB 729 KROIISVAFTVOAAAEITLSEVA 750

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RESULT 5
US-09-044-668-2
: Sequence 2, Application US/09044668
: Patent No. 6150508
: GENERAL INFORMATION:
:   APPLICANT: Murphy, Gerald P.
:   APPLICANT: Boynton, Alton L.
:   APPLICANT: Holmes, Eric H.
:   APPLICANT: Tino, William Thomas
:   TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC
:   TITLE OF INVENTION: FOR THE EXTRACELLULAR DOMAIN OF PROSTATE-SPECIFIC
:   TITLE OF INVENTION: MEMBRANE ANTIGEN

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; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds, LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: FASTSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/044.668
 ; FILING DATE: 18-MAR-1998
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Baldwin, Geraldine F
 ; REGISTRATION NUMBER: 31,232
 ; REFERENCE/DOCKET NUMBER: 8511-0013-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-493-4935
 ; TELEFAX: 650-493-5556
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 750 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 6150508e
 ; US-09-044-668-2

Query Match 98.2%; Score 2288; DB 3; Length 750;
 Best Local Similarity 98.0%; Pred. No. 1.8e-214;
 Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY	1	MGSAPDPSWMSGLKVSYPGFTGNFSTQKVMHISTNEVRIYVIGTLGA	60
DB	309	MGSAPDPSWMSGLKVSYPGFTGNFSTQKVMHISTNEVRIYVIGTLGA	368
QY	61	DRYVILGGHDSWVEGGIDPOGSAVHETVRSFGLTKEGMRPRTILFASWDAEE	120
DB	369	DRYVILGGHDSWVEGGIDPOGSAVHETVRSFGLTKEGMRPRTILFASWDAEE	428
QY	121	LGSTWADNSRLLOERGVAYINADSSIEGNTTLAVDCTPLMYSLVNLTKEKSPD	180
DB	429	LGSTWADNSRLLOERGVAYINADSSIEGNTTLAVDCTPLMYSLVNLTKEKSPD	488
QY	181	EKSLYESWTKKSPPEFSGMPRIKSLGSGNDFEYFORLGIASGRARYTNWETN	240
DB	489	EKSLYESWTKKSPPEFSGMPRIKSLGSGNDFEYFORLGIASGRARYTNWETN	548
QY	241	YPLYSVYETVELVEKFTYDPMKYLITVAOYRGAVFELANSIVLPDCRDYAV	300
DB	549	YPLYSVYETVELVEKFTYDPMKYLITVAOYRGAVFELANSIVLPDCRDYAV	608
QY	301	DKIYISMKHPQEMKTYISFDSLSAYKNTFELASKSEERLQDPDKSNPIVLR	360
DB	609	DKIYISMKHPQEMKTYISFDSLSAYKNTFELASKSEERLQDPDKSNPIVLR	668
QY	361	MELEAFIDPLGLPRPRYRHVITAPSSHNKYAGSFPGIYDALDIESKVP	420
DB	669	MELEAFIDPLGLPRPRYRHVITAPSSHNKYAGSFPGIYDALDIESKVP	728
QY	421	KROIYVAAFVYQAAAEITLSEVA 442	
DB	729	KROIYVAAFVYQAAAEITLSEVA 750	

RESULT 6
 US-08-705-477E-2
 ; Sequence 2, Application US/08705477E
 ; Patent No. 6569432
 ; GENERAL INFORMATION:
 ; APPLICANT: Israeli, Ron S
 ; APPLICANT: Heston, Warren D.W.
 ; APPLICANT: Fair, William R.
 ; APPLICANT: Overfelli, Quathek
 ; APPLICANT: Pinto, John
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 1769/41426-G
 ; CURRENT APPLICATION NUMBER: US/08/705.477E
 ; CURRENT FILING DATE: 1996-08-29
 ; NUMBER OF SEQ ID NOS: 128
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 750
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-08-705-477E-2

Query Match 98.2%; Score 2288; DB 4; Length 750;
 Best Local Similarity 98.0%; Pred. No. 1.8e-214;
 Matches 433; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY	1	MGSAPDPSWMSGLKVSYPGFTGNFSTQKVMHISTNEVRIYVIGTLGA	60
DB	309	MGSAPDPSWMSGLKVSYPGFTGNFSTQKVMHISTNEVRIYVIGTLGA	368
QY	61	DRYVILGGHDSWVEGGIDPOGSAVHETVRSFGLTKEGMRPRTILFASWDAEE	120
DB	369	DRYVILGGHDSWVEGGIDPOGSAVHETVRSFGLTKEGMRPRTILFASWDAEE	428
QY	121	LGSTWADNSRLLOERGVAYINADSSIEGNTTLAVDCTPLMYSLVNLTKEKSPD	180
DB	429	LGSTWADNSRLLOERGVAYINADSSIEGNTTLAVDCTPLMYSLVNLTKEKSPD	488
QY	181	EKSLYESWTKKSPPEFSGMPRIKSLGSGNDFEYFORLGIASGRARYTNWETN	240
DB	489	EKSLYESWTKKSPPEFSGMPRIKSLGSGNDFEYFORLGIASGRARYTNWETN	548
QY	241	YPLYSVYETVELVEKFTYDPMKYLITVAOYRGAVFELANSIVLPDCRDYAV	300
DB	549	YPLYSVYETVELVEKFTYDPMKYLITVAOYRGAVFELANSIVLPDCRDYAV	608
QY	301	DKIYISMKHPQEMKTYISFDSLSAYKNTFELASKSEERLQDPDKSNPIVLR	360
DB	609	DKIYISMKHPQEMKTYISFDSLSAYKNTFELASKSEERLQDPDKSNPIVLR	668
QY	361	MELEAFIDPLGLPRPRYRHVITAPSSHNKYAGSFPGIYDALDIESKVP	420
DB	669	MELEAFIDPLGLPRPRYRHVITAPSSHNKYAGSFPGIYDALDIESKVP	728
QY	421	KROIYVAAFVYQAAAEITLSEVA 442	
DB	729	KROIYVAAFVYQAAAEITLSEVA 750	

RESULT 7
 US-08-705-477E-101
 ; Sequence 101, Application US/08705477E
 ; Patent No. 6569432
 ; GENERAL INFORMATION:
 ; APPLICANT: Israeli, Ron S
 ; APPLICANT: Heston, Warren D.W.
 ; APPLICANT: Fair, William R.
 ; APPLICANT: Overfelli, Quathek
 ; APPLICANT: Pinto, John
 ; TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 1769/41426-G
 ; CURRENT APPLICATION NUMBER: US/08/705.477E

;; CURRENT FILING DATE: 1996-08-29
;; NUMBER OF SEQ ID NOS: 128
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 101
;; LENGTH: 693
;; TYPE: PRT
;; ORGANISM: Homo Sapiens
US-08-705-477E-101

Query Match 97.9%; Score 2281; DB 4; Length 693;
Best Local Similarity 97.7%; Pred. No. 7.5e-214;
Matches 432; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGSSAPPDSSMRSLKYSYVNGPFTGNFSTOKYKMHISTNEVTRIYNYIGTLRGAVEP 60
DB 252 MGSSAPPDSSMRSLKYSYVNGPFTGNFSTOKYKMHISTNEVTRIYNYIGTLRGAVEP 311
QY 61 DRYVILGHRDQVFGGIDPQSGAAYVHETVRSFGTLKKGWRPRTTILFASMDAEFGL 120
DB 312 DRYVILGHRDQVFGGIDPQSGAAYVHETVRSFGTLKKGWRPRTTILFASMDAEFGL 371
QY 121 LGSTEMADNSRLIOERGVAIYNADSSIEGNYTLRVCTPLMYSLYNLTRELKSPDEGF 180
DB 372 LGSTEMADNSRLIOERGVAIYNADSSIEGNYTLRVCTPLMYSLYNLTRELKSPDEGF 431
QY 181 EGKSLYESWTKKSPSPFSGMPRIKSLGSGNDEFEVFORLGIASGRARYTKNMETNFKFSG 240
DB 432 EGKSLYESWTKKSPSPFSGMPRIKSLGSGNDEFEVFORLGIASGRARYTKNMETNFKFSG 491
QY 241 YPLHYSYETVELVEKYEDPMFKYHLTVAOVRGGMVELANSIVLPDCRDYAVVLRKYA 300
DB 492 YPLHYSYETVELVEKYEDPMFKYHLTVAOVRGGMVELANSIVLPDCRDYAVVLRKYA 551
QY 301 DKTYINSMKHPQEMKTYSLSPDSLFSYVKNFTETLASFESRLODFDQSNPTLLRMNDOL 360
DB 552 DKTYINSMKHPQEMKTYSLSPDSLFSYVKNFTETLASFESRLODFDQSNPTLLRMNDOL 611
QY 361 MFLERAFIDPLGDRPFRHYVYAPSSHNKYAGESPFGIYDALFDIESKVPKANGDV 420
DB 612 MFLERAFIDPLGDRPFRHYVYAPSSHNKYAGESPFGIYDALFDIESKVPKANGDV 671
QY 421 KROIYVAFTVOAAAEFTLSEVA 442
DB 672 KROIYVAFTVOAAAEFTLSEVA 693

RESULT 8
US-08-547-197-1
; Sequence 1, Application US/08547197
; Patent No. 5691157
; GENERAL INFORMATION:
; APPLICANT: Gong, Joseph K.
; APPLICANT: Glomski, Chester A.
; TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
; TITLE OF INVENTION: EXPOSURE TO RADIATION OR RADIOMETRIC AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/547,197
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

;; NAME: Rogalsky, Peter
;; REGISTRATION NUMBER: 38,601
;; REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (716) 263-1600
;; TELEFAX: (716) 263-1634
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 622 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-547-197-1

Query Match 19.1%; Score 445.5; DB 1; Length 622;
Best Local Similarity 26.0%; Pred. No. 1.2e-34;
Matches 118; Conservative 89; Mismatches 180; Indels 67; Gaps 11;

QY 1 MGSSAPPDSSMRSLKYSYVNGPFTGNFSTOKYKMHISTNEVTRIYNYIGTLRG 56
DB 211 MEGNCPPSWNIDSECK--LELSON-----QNVKLVNNVYLKETRLINFGYIKG 257
QY 57 AVEPDYVILGHRDQVFGGIDPQSGAAYVHETVRSFG--TLKKGWRPRTTILFASMDA 115
DB 258 YEEPDYVILGHRDQVFGGIDPQSGAAYVHETVRSFG--TLKKGWRPRTTILFASMDA 317
QY 116 EERGLDSTEMADNSRLIOERGVAIYNADSSIEGNTLVDCPLMYSLYNLTRELKLS 175
DB 318 GDYGAVPTLMELEYSLSLHLKAFYIINDKLVIGTGNFVYASAPLTYTLGKIMQDVKH 377
QY 176 PDEGFEKSLY--ESWTKKSPSPFSGMPRIKSLGSGNDEFEVFORLGIASGRARYTKNW 233
DB 378 P---IDCKYILKRNNTMSK-----IEELSDNAPFLFAYSGIRAVSFCFED 422
QY 234 EYKFSQPLYHSYETVELVEKYEDPMFKYHLTVAOVRGGMVELANSIVLPDCRDY 293
DB 423 ---EDYPLGTLDYELLIQVPOLDNOMVFAAIVAGOFIKTLNHDIELFDYBMYN 477
QY 294 VVLRKYADKTYINSMKHPQEMKTYSLSPDSLFSYVKNFTETLASFESRLODFDQSNPTLL 353
DB 478 SKLLSPKDLNQK---ADIKDGLSLQWLYSARGYFRATSLTDFDFAEETNRFV 533
QY 354 RNMNDOLMFLERAFIDPLGDRPFRHYVYAPSSHN-----KYAGESPFGIYDALF 405
DB 534 REINDRIMKYEYHLSPYVSRESFRKHFIMGSSHTLSALVETLRLRKNITAFNFTLF 593
QY 406 DIESKVPKANGDVKROIYVAFTVOAAAEFTLS 439
DB 594 -----RQDLALATWTIOGVANALS 612

RESULT 9
US-08-957-940-1
; Sequence 1, Application US/08957940
; Patent No. 6132981
; GENERAL INFORMATION:
; APPLICANT: Gong, Joseph K.
; APPLICANT: Glomski, Chester A.
; TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
; TITLE OF INVENTION: EXPOSURE TO RADIATION OR RADIOMETRIC AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,940
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,940
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/547,197
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Rogalsky, Peter
REGISTRATION NUMBER: 38,601
REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-957-940-1

Query Match 19.1%; Score 445.5; DB 3; Length 622;
Best Local Similarity 26.0%; Pred. No. 1.2e-34;
Matches 118; Conservative 89; Mismatches 180; Indels 67; Gaps 11;

OY 1 MGSAPP---DSWRSGLKVSINVGPGFTGNSIQKVMHISTNEVRIYVIGTGL 56
DB 211 MGNCPSPSNNIDSSCK--LELSON-----QNVALLVNNVYKRIINIEGVIG 257
OY 57 AVEPRRYVYLGGHRSWVFGIDPOSGAAVHEIVRSFG-TLKEGWRPRRTILFASWDA 115
DB 258 YEPRRYVYVGAORAMGPGVAKSSVGTGLTLKLAQVESDMISKDGFSPRSIIIFASMTA 317
OY 116 EEEGLIGSTEMAEDNSRLQERGVAYINADSSIEGNYTLRVDCPTLMYSLVNLTKELKS 175
DB 318 GDYGVAGPTEMELEGYLSHLKAFYIINDKAVYLGTSNFKVSAFLYTLKIMODVH 377
OY 176 PDEGEGKSLY--ESWTKSPSPESGMPRISKLSGNDFEYFQRLGASGRARYTKNM 233
DB 378 P--IDGKLYLRNSNMISK-----IEELSLDNAAPFLAVSGIPAVSFCED- 422
OY 234 EINKSGYPLHYSVETVLEVEKFDPMKHYIAQVGVGNVFEELANSIVLPDCRDYA 293
DB 423 -----EDPYLGTKLDTYEILLQKVPQNLQWVRTAAEVAAGOFILKILTHDIELLDEYEMN 477
OY 294 VVLRKYADKIYINSMKHPQEMKTYSLSPDLSFSAVKNFTEIASKESERLQDDEKSNPIL 353
DB 478 SKLSGFMKDLNQF---ADIKDGLSLQWLYSARGDYFRATSRKLTIDPHNAEKTRRYA 533
OY 354 RMANQMLERAFIDPLGLPDRPFYRHVAYPSSHN-----KYASESPGIYDALF 405
DB 534 REINRIMKVEYHFLSPYVSPRESPEHFHFGSGHTLSALVENLRLOKNTATFNETLF 593
OY 406 DIESKVDPSKAMGDVKKQISVAAPFYQAAAEFLS 439
DB 594 -----RNQIALATWTIQQVANAALS 612

RESULT 10
US-08-547-197-2
Sequence 2, Application US/08547197
Patent No. 5691157
GENERAL INFORMATION:
APPLICANT: Gong, Joseph K.
TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
EXPOSURE TO RADIATION OR RADIOMIMETIC AGENTS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/547,197
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rogalsky, Peter
REGISTRATION NUMBER: 38,601
REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-547-197-2

Query Match 18.2%; Score 425; DB 1; Length 760;
Best Local Similarity 26.5%; Pred. No. 1.6e-32;
Matches 110; Conservative 93; Mismatches 172; Indels 40; Gaps 11;

OY 31 TOKVMHISTNEVRIYVIGTGLGAVPEPRRYVYLGGHRSWVFGIDPOSGAAVHEI 90
DB 370 SKAVKLYVSNVLAKEKILNIEFVIGFVPEPDHYVYVGAORAMGPGAAKSGVGTALLKL 429
OY 91 VRSFGLT-KKEGWRPRRTILFASWDAEEFGLIGSTEMAEDNSRLQERGVAYINADSSIE 149
DB 430 AQMFSDMYLKDFQPSRSIIIFASWAGDFGSGVATEMELEGYLSHLKAFYIINDKAVL 489
OY 150 GNYTLRVDCPTLMYSLVNLTKELSPDEGEGKSLYE--SWTKSPSPESGMPRISKL 207
DB 490 GTSNFKVSAPLTYLLEKTMQNVKHP--VTGQFLYDQSMASK-----VERL 535
OY 208 GSGNDFEYFQRLGASGRARYTKNMETNKFSGYPLHYSVETV-ELVEKFDPMKHYHL 266
DB 536 TLDNAAPFLAVSGIPAVSFCED-----TDYVLTGTMDTYKELLERIP- LNKAR 588
OY 267 TVAQVGVGNVFEELANSIVLPDCRDYAVVLRKYADKIYINSMKHPQEMKTYSLSPDLS 326
DB 589 AAEEVAGQFVILKTHDVELINDYERYNSQLSFVBDLNG---YRADIKEMGLSLQWLYS 644
OY 327 AVKNFTEIASKSEHLDQFDSNPIILLRMANQMLERAFIDPLGLDRPFYRHVAYIAP 386
DB 645 AAGDFFRATSRITTDGNAEKTRDFVKKLNDRVARVEYHFLSPYVSPRESPEFRHVEWGS 704
OY 387 SSHNKYAGESPFIYDALFDEIESKVDPSKAMGDV--KKQISVAAPFYQAAAEFLS 439
DB 705 GSH-----TLPAL---LENLKLKRNQNGAFNETIFRNQALATYTIQGAANAALS 750

RESULT 11
US-08-957-940-2
Sequence 2, Application US/08957940
Patent No. 6132981
GENERAL INFORMATION:
APPLICANT: Gong, Joseph K.
TITLE OF INVENTION: A METHOD FOR DETECTING A MAMMAL'S PRIOR
EXPOSURE TO RADIATION OR RADIOMIMETIC AGENTS
NUMBER OF SEQUENCES: 2

```

CORRESPONDENCE ADDRESS:
ADDRESS: 1000 N. Main Street, Suite 100,
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,940
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/547,197
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Rogalsky, Peter
REGISTRATION NUMBER: 38,601
REFERENCE/DOCKET NUMBER: 19226/580 (R-5228)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1634
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-957-940-2
```

```

Query Match      18.2%; Score 425; DB 3; Length 760;
Best Local Similarity 26.5%; Pred. No. 1.6e-32;
Matches 110; Conservative 93; Mismatches 172; Indels 40; Gaps 11;
```

```

QY 31 TOKVHHSTNEVTIRYVIGTLRGAVPEPDRYVILGSHDQSVFPGIDPOGAAYVHET 90
DB 370 SKNVKLTGNSVLEKIRILNFGVKGPEPDHYVVGAGQDANGPQAASGVGTALLKL 429
QY 91 VRSFGTL-KKEGMRPRTILFASWDAEEFGLGSTEWAEDNSRLQERGVAAYINADSSIE 149
DB 430 AQHFSQMLKDGQPSRSIIIFASMSAGDGSVATMLEBYSLSLHAKATTYINLDKAVL 489
QY 150 GNTLVDCPLMYSLVYNLTRELKSPDEGFEKSLYE-SWTKKSPSPFSGMPRI SKL 207
DB 490 GTSNFRVSASPLLYLTLEKTMQWVHP-VTGQPLFYODSNMWSK-----VEKL 535
QY 208 GSGNDEVEFQRLGASGRARYTKMETNKFSGYPLHSHVLEY-ELVEKFIYPMKRYHL 266
DB 536 TLDNAAPFLAVSGIYAVSFCFED-----TDYPLGTMDYKLEIETIPE-LNKVAR 588
QY 267 TVAQVAGWGFELANSIVLPECDRYAVYLRYADRYINISMKHPQEMKTYSPFSLFS 326
DB 589 AAEEVAGQFYIKITHEVELNDYERINSQLSLTFVRDLG----YRADIKEMGSLQMTLS 644
QY 327 AVANFTELASKESERLQDFDKSNPILLRMNDQMLERAFIDPLGLPDPFYRHVYAP 386
DB 645 ARGDFFRATSRILTTDGNNAEKTRDFYMKKILNDRVMEVYHFLSPVSPKESPRHFWGS 704
QY 387 SSNNKYGASFPFIYALFDIESKVPDSKAMGV--KROISVAAYVQAAETLS 439
DB 705 GSH-----TLPAL---LENLKLKRONNGAFNETLFRNDLALATWTIOGAANLS 750
```

```

RESULT 12
US-09-079-955-2
Sequence 2, Application US/09079955A
Patent No. 6465209
GENERAL INFORMATION:
```

```

APPLICANT: Alexander Blinkovsky
APPLICANT: Kimberly Brown
APPLICANT: Elizabeth Golightly
APPLICANT: Tony Byun
APPLICANT: Thomas Mathiasen
APPLICANT: Lene V. Kofoed
APPLICANT: Mikio Fujii
APPLICANT: Chigusa Shizuoka
TITLE OF INVENTION: Methods for Producing Protein
FILE REFERENCE: 5253,500-US
CURRENT APPLICATION NUMBER: US/09/079,955A
CURRENT FILING DATE: 1998-05-15
NUMBER OF SEQ. ID NOS: 11
SOFTWARE: FastSeq for Windows Version 3.0
SEQ. ID NO 2
LENGTH: 496
TYPE: PRT
ORGANISM: Aspergillus oryzae
US-09-079-955-2
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```

Query Match      5.7%; Score 133.5; DB 4; Length 496;
Best Local Similarity 25.5%; Pred. No. 0.00024;
Matches 51; Conservative 29; Mismatches 87; Indels 33; Gaps 9;
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```

QY 34 VKMHSTNEVTIRYVIGTLRGAVPEPDRYVILGSHDQSVFPGIDPOGAAYVHETVR 92
DB 214 VDLWDSKQENRTTYVNAQTGK-DPNNVVALGHTDSVEAGPGIN-DDGSGIISNLVY 271
QY 93 SFGLTKKEGMRPRTILFASWDAEEFGLGSTEWAEDNSRLQERGVAAYINADSSIEGNY 152
DB 272 AKALQ---YSKNAVAFLEWFAEEFGLGSNYYVSHLNATELNKIRILNFDMIASPNY 328
QY 153 TLAVDCPLMYSLVYN---LTRELKSPDEGFEKSLYESWTKKSPSP-----ESGAPRIS 205
DB 329 AL-----MIYGDGSAFNQSGPAGSAQIEKLEFDYDSDILPHIPTQDGR----- 374
QY 206 KLGSGNDEVEFQRLGIASG 225
DB 375 -----SDYFAFILN-GIPSG 388
```

```

RESULT 13
US-09-330-095-1
Sequence 1, Application US/09330095
Patent No. 6127161
GENERAL INFORMATION:
APPLICANT: Kikkoman Corporation
TITLE OF INVENTION: Leucine Aminopeptidase Gene, Recombinant DNA, and
FILE REFERENCE: PH-672
CURRENT APPLICATION NUMBER: US/09/330,095
CURRENT FILING DATE: 1999-06-11
EARLIER APPLICATION NUMBER: JP-164611/1998
NUMBER OF SEQ. ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ. ID NO 1
LENGTH: 481
TYPE: PRT
ORGANISM: Aspergillus sojae
US-09-330-095-1
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Query Match      5.6%; Score 131.5; DB 3; Length 481;
Best Local Similarity 25.5%; Pred. No. 0.00036;
Matches 51; Conservative 29; Mismatches 87; Indels 33; Gaps 9;
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```

QY 34 VKMHSTNEVTIRYVIGTLRGAVPEPDRYVILGSHDQSVFPGIDPOGAAYVHETVR 92
DB 199 VDLWDSKQENRTTYVNAQTGK-DPNNVVALGHTDSVEAGPGIN-DDGSGIISNLVY 256
QY 93 SFGLTKKEGMRPRTILFASWDAEEFGLGSTEWAEDNSRLQERGVAAYINADSSIEGNY 152
```

```

Db      257  ANKLQI---YSVKNANARFLFWTAEEFGILGSNYVSHLNLATLNLKIRLYLNFDMIASPNY 313
OY      153  TLRVDCITPLMTSLVYN---LTKELKSPDDGCFECKSLYESWTKKSPD-----EFGMPRIS 205
Db      314  AL-----MITYDGSAPFNOSGPASAOIEKLFEDYYSIDPLPHIPTQFDGR---- 359
OY      206  KLGSGNDEVEYFQRLGIASG 225
Db      360  -----SDYEAFILN-GIPAG 373

RESULT 14
US-09-482-273-120
; Sequence 120, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273
; EARLIER FILING DATE: 2000-01-13
; EARLIER APPLICATION NUMBER: PCT/US99/15849
; EARLIER FILING DATE: 1999-07-14
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,922
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/092,956
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (473)
; OTHER INFORMATION: xaa equals stop translation
US-09-482-273-120

Query Match          5.3%; Score 122.5; DB 4; Length 473;
Best Local Similarity 32.1%; Pred. No. 0.0027;
Matches 27; Conservative 18; Mismatches 34; Indels 5; Gaps 2;

OY      45  TRIYVNGTGLRGAVEPDPRVYILGGRDSSWF--GGIDPQSGAAVYHETVRSFGTLKKEGW 102
Db      266  TDSNTVTAETIGSKYPPQVYLVSGHDSWVGGCANDGGGAFISWE---ALSIRKDLGL 322
OY      103  RPRRTILFASMDAEFGILGSTEW 126
Db      323  RPKRTLRLVMTAAEAGGVCAGAFQY 346

RESULT 15
US-09-252-991A-18292
; Sequence 18292, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18292
; LENGTH: 584
; TYPE: PRT

```

```

: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18292

Query Match      5 2% Score 121.5; DB 4; Length 584;
Best Local Similarity 25.9%; Pred. No. 0.0047;
Matches 60; Conservative 41; Mismatches 84; Indels 47; Gaps 14.

OY    10 SWRGSLLK---SYVNGPGFGTGNFSTQKKMH--LHSTSEVTIRIVNVG--TLRGAVEPDRY 63
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    284 SYEGGIPIFYFTTYDNGVAMS---QTDPDQLHLVDVYARKKTETYNVAEFRGG--NPNVV 338

.OY   64 VILGGHRDSWVEFG--IDPQGAAYVHETVRSFCTLKECKMRPRRTITLRASMDAEERGL 120
       ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    339 VMWGHHLS-VVEEGGINDSGSSAOLE---MAVLAKA-LPYNKVRFFMWGGEERGL 392

OY    121 LGSTEMADNSRLLOERGVATINMDSSTIEGWYTILRVDTPLMYSLVYLITELKSPPDEGF 180
       ||| : | : | : | : | | | | | | | | | | | | | | | | | | | | | |
Db    393 VGSTHYVNLAPEEKKKIKALINFDMIGSPNNG-----NFYYDGSDSDFGL 438

OY    181 EG-----KSLYESMTKSSPSPEFSGPRISSKLISGNDFEVFQORTLIASG 225
       | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db    439 QGPSRAIAERLFETVYFLRLR-GQGSEG----TEIDFRDYAEFFMS-GIAGF 484

```

Search completed: October 4, 2003, 23:26:47
Job time : 37 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2003, 23:09:12 ; Search time 39 Seconds
(without alignments)
1089.912 Million cell updates/sec

Title: US-09-973-382C-2
Perfect score: 2329
Sequence: 1 MGSAAPPDSSWRGSLKVSYN.....QISVAFTVQAAETLSEVA 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2288	98.2	750	2 A56881	prostate-specific
2	631.5	27.1	751	2 T30154	hypothetical prote
3	579	24.9	703	2 T47631	peptidase-like pro
4	545.5	23.4	1483	2 T19751	hypothetical prote
5	445.5	19.1	622	2 A34549	transferrin recept
6	435	18.7	763	1 S29548	transferrin recept
7	426	18.3	760	1 JXHU	transferrin recept
8	424.5	18.2	757	2 A48592	transferrin recept
9	413.5	17.8	776	1 JH0570	transferrin recept
10	399	17.1	811	2 S57149	probable membrane
11	355	15.2	794	2 T40289	hypothetical prote
12	252	10.8	280	2 E85075	probable peptidase
13	240.5	10.3	809	2 S67153	probable membrane
14	179.5	7.7	783	2 S67158	secretory protein
15	173	7.4	529	2 G82759	hypothetical prote
16	157	6.7	467	2 G87564	aminopeptidase, pr
17	152.5	6.5	430	2 A87634	peptidase, M20/M25
18	148	6.4	501	2 C82414	aminopeptidase VCA
19	140.5	6.0	284	2 S66427	aminopeptidase (EC
20	139.5	6.0	504	2 S24314	bacterial leucyl a
21	133	5.7	374	2 S69699	hypothetical prote
22	130.5	5.6	500	2 H70629	probable AMINOPEPT
23	126.5	5.4	493	2 T46974	leucyl aminopeptid
24	121.5	5.2	536	2 B83278	probable aminopept
25	118.5	5.1	455	2 S39653	aminopeptidase hom
26	117	5.0	609	2 JC7819	metalloprotease
27	116	5.0	893	2 T18271	hypothetical prote
28	116	5.0	1123	2 T18270	hypothetical prote
29	113.5	4.9	647	2 A83606	hypothetical prote

30	113	4.9	468	2 F87359	leucine aminopepti
31	112	4.8	411	2 B90701	allantoate amidohy
32	112	4.8	411	2 E85551	probable hydantoin
33	111	4.8	537	2 A54134	aminopeptidase y (
34	108	4.6	411	1 C64783	probable N-cardamy
35	107.5	4.6	488	2 A87569	peptidase M20/M25/
36	107.5	4.6	1447	2 S63669	UDPglucose-glycopr
37	107	4.6	980	2 T24556	hypothetical prote
38	106.5	4.6	449	2 H97249	protein containing
39	106.5	4.6	571	2 H87600	hypothetical prote
40	106	4.6	1481	2 S28669	pullulanase (EC 3.
41	105	4.5	2957	2 T33152	hypothetical prote
42	103	4.4	816	2 C83424	assimilatory nitri
43	103	4.4	855	2 A71223	hypothetical prote
44	102.5	4.4	759	2 J01045	aryphorin precurs
45	101.5	4.4	704	2 T01772	hypothetical prote

ALIGNMENTS

RESULT 1
A56881
prostate-specific membrane antigen - human
C/Species: Homo sapiens (man)
C/Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-2000
C/Accession: A56881
R/Israeli, R.S.; Powell, C.T.; Fair, W.R.; Heston, W.D.
Cancer Res. 53, 227-230, 1993
A/Title: Molecular cloning of a complementary DNA encoding a prostate-specific membra
A/Reference number: A56881; MUID:93113576; PMID:8417812
A/Accession: A56881
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-750 <ISR>
A/Cross-references: GB:M99487; NID:q190663; PIDN:AAA60209.1; PID:q190664
A/Experimental source: prostatic carcinoma cell line LNCaP
A/Note: sequence extracted from NCBI backbone (NCBIN:121724, NCBI:P.121725)
C/Superfamily: transferrin receptor
C/Keywords: surface antigen; transmembrane protein

Query Match	Score	2288	DB 2	Length	750
Best Local Similarity	98.0%	Pred. No. 1.8e-163			
Matches	433	Conservative	6	Mismatches	3
		Indels	0	Gaps	0
QY	1	MGSAAPPDSSWRGSLKVSYNVGGFTGNFSTQVKMHNISTNEVTRIVYVIGTLRGAVEP	60		
DB	309	MGSAAPPDSSWRGSLKVPYNVGGFTGNFSTQVKMHNISTNEVTRIVYVIGTLRGAVEP	368		
QY	61	DRVYVILGHRDSWVFGCIPDQSGAAYVHETVRSFGTLKREGMRPRRTILFASWDAAEFGL	120		
DB	369	DRVYVILGHRDSWVFGCIPDQSGAAYVHETVRSFGTLKREGMRPRRTILFASWDAAEFGL	428		
QY	121	LGSTWAEEDNSRLLOERGAAYINADSSIEGNTYLRYDCTPLMYSLVYNTLKEKSPDEGF	180		
DB	429	LGSTWAEEDNSRLLOERGAAYINADSSIEGNTYLRYDCTPLMYSLVYNTLKEKSPDEGF	488		
QY	181	EGKSLYESWTKKSPSPFSGMPRIKLGSGNDFEVFFQRLGIASGARATTKMNETKFSFG	240		
DB	489	EGKSLYESWTKKSPSPFSGMPRIKLGSGNDFEVFFQRLGIASGARATTKMNETKFSFG	548		
QY	241	YPLVHSVYETVELVEKFDYDPMFKYHLTVAVOVRGAWFEELANSIVLPFDDRDVAAYVLRKA	300		
DB	549	YPLVHSVYETVELVEKFDYDPMFKYHLTVAVOVRGAWFEELANSIVLPFDDRDVAAYVLRKA	608		
QY	301	DKTYINSMKHPQEMKTYSLFSDSLFSAVKNFTETIASKFSERLODFDKSNPILLRMANNOL	360		
DB	609	DKTYINSMKHPQEMKTYSLFSDSLFSAVKNFTETIASKFSERLODFDKSNPILLRMANNOL	668		
QY	361	MTLEKAFIDPLGIDPDPFRHRYVLAASSHNKTAGESFPGLTYDALPDESKVDPKAMGCV	420		
DB	669	MTLEKAFIDPLGIDPDPFRHRYVLAASSHNKTAGESFPGLTYDALPDESKVDPKAMGCV	728		


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Db      320 MKGDA-VNADEFGKLNVTYRYGPGGLINN---OKLRVYVAENEERSVIYVELLSRLNLF 375
Oy      45  TRIVAVIGTLRCAVPPDRYVILGHRDSVVEGIDIPGSAAYVHEVRSFGLLKKE-GWR 103
Db      376 RRIQNIIMGKIKSGSPDDKFEVLVSNHYDAWTVGAVPNSGTSFLLVESRLKQYQONQGM 435
Oy      104 PARTLLFASWDAEEFGILGSTEMADNSRLLOERGAAYINADSSIEGNTYLLVDCPTLMY 163
Db      436 PARSLIFAMDMDEEGLIGLSTFEAEERYQLQLMRAVAVINMD-LIGGNTLLGLNSPIYA 494
Oy      164 SLVYNLTRELKSPD--EGFEG-KSLYESWTKKSPSPFSGMRISKL-GSGNDFEYFQR 219
Db      495 NVLRSAANAANVEQNPTEMEQGRKTLYDSWKYAPSKNNRSTHPYORIPAGSGDHLPEFDY 554
Oy      220 LGI-----ASGRARYTKNMETNKFSGPLYHSHVETELVEKRYDDPMFKHLYVAQVR 272
Db      555 LGPIVIFFTSSLDAPPT-----YPIVHTIYETPYLLEIMDPGKYHKAKIAGMF 604
Oy      273 GGMVEFLANSIYLPDPCRDYAVVLRKRYADKIYNISMKHPQEM-KTYSL--SPDSLFSAYK 329
Db      605 IECILKFTMSKTLPLPDNL-----MDSIFEYLPKLEDRKLTKMLTKTKDYLLDAOK 658
Oy      330 NFEIASKFSERLQDPKSN-----PILLR-MNDQLMFLERAFIDPLGLPDRPFYRH 381
Db      659 OFKLQKTVLELSEIYQRRNVSKLEELPFGSHVDINNRLIEFEKCFINPHGAIGNQARH 718
Oy      382 VYIYASSHNKYGSEFPGLYDALFDIESKVDPSKMGDVKROIYSAAFYVQA 434
Db      719 VLEHSPDMWYDGDALISQVHDLISKISNST-SKEGLKSLQLAKEIALVNVA 770

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RESULT 5

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A34549
transferrin receptor - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Aug-1999
C:Accession: A34549
R:Roberts, K.P.; Griswold, M.D.
Mol. Endocrinol. 4: 531-542, 1990
A:Title: Characterization of rat transferrin receptor cDNA: the regulation of transferrin
A:Reference number: A34549; MUID:91125359; PMID:2126342
A:Accession: A34549
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-622 <ROB>
A:Cross-references: GB:M58040; NID:9207463; PIDN:AAA42273.1; PID:9207464
C:Superfamily: transferrin receptor
C:Keywords: receptor; transmembrane protein

```

```

Query Match      19.1%: Score 445.5; DB 2: Length 622;
Best Local Similarity 26.0%: Pred. No. 1.9e-25;
Matches 118; Conservative 89; Mismatches 180; Indels 67; Gaps 11;

Oy      1  MGSGAP-----DSWRGSLKSYNVNGPGFTGNFSTQVKMHIHSTNEVRIYVIGTLRG 56
Db      211 MGCNCPSPMNISSCK--LELSQN-----QNVKLVYNNVLAKEIRILINIGVIRG 257
Oy      57  AVEPRRIYILGHRDSWVFGIDIPGSAAYVHEVRSFG-TLKSGMRPRRTILFASWDA 115
Db      258 YEPRRIYVYQORAWGPGVAKSSVGTGLLKLQAVESDMISKDGFSPRSRIIFASWTA 317
Oy      116 BEFGILGSTEMADNSRLLOERGAAYINADSSIEGNTYLLVDCPTLMYSLVYNLTRELK 175
Db      318 GDYGVAGPEWLEGLSLILKAFYINLDKVVLTGSNEKVASASPLTLTKKIMQDVAKH 377
Oy      176 PDEGEGKSLY--ESWTKKSPSPFSGMRISKLSGNDFEYFQRLGIASGRARYTKNM 233
Db      378 P---IDGKVLNNSMWISK-----IDELSLDNAAFFLAVSGIPAVSPFCED- 422
Oy      234 EYNKSGIPLVSHVETELVEKRYDDPMFKHLYVAQVRGGMVFLANSIYLPDPCRDYA 293
Db      423 -----EDYPYLGTKLDYELIQLQKVPOLNQWRTAAEAVAGPFIKLTHDIELTLYEYMN 477

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Oy      294 VVLRKYADKIYNISMKHPQEMKTSLSFDSLFSAYKNFTEIASKESERLODPKSNPILL 353
Db      478 SKLLEFMDLQNFK----ADIKMDGLSLQWLYXSAAGDFRAISRLLTDDHNAEKNNRFWM 533
Oy      354 RNMNDQLMFLERAFIDPLGLPDRPFYRHVYAPSSHN-----KYAGESPGLYDALF 405
Db      534 REINDIRIMKVEYHFLSPYSPRESPFRHIFMGSGSHTLALVENLRQLKNTAFNETLF 593
Oy      406 DIESKVDPSKMGDVKROIYSAAFYVQAARETL 439
Db      594 -----RNDIALATWITQGVANALS 612

```

RESULT 6

```

S29548
transferrin receptor - mouse
N:Alternate names: CD71; p90
N:Contains: 85K serum transferrin receptor
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29548; A26735; D24550; I49662
R:Rothemberger, I.S.; Domingo, D.L.; Thomas, M.L.; Chain, A.
submitted to the EMBL Data Library, January 1991
A:Reference number: S29548
A:Accession: S29548
A:Status: preliminary

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A:Molecule type: mRNA
A:Residues: 1-763 <PRO>
A:Cross-references: EMBL:X57349; NID:954914; PIDN:CAA40624.1; PID:954915
R:Rothemberger, S.; Iacopetta, B.J.; Kuhn, L.C.
Cell 49, 423-431, 1987
A:Title: Endocytosis of the transferrin receptor requires the cytoplasmic domain but
A:Reference number: A26735; MUID:87187639; PMID:3568132
A:Accession: A26735
A:Molecule type: protein
A:Residues: 1-82 <ROT>
R:Grego, B.; Van Driel, I.R.; Stearne, P.A.; Goding, J.W.
Eur. J. Biochem. 148, 485-491, 1985
A:Reference number: A24550; MUID:85203852; PMID:2986964
A:Accession: D24550
A:Molecule type: protein
A:Residues: 7-19;158-175,'X',177-179;'DESL','AY',189,'IEN',193,'FXEF',195;196,197-208
A:Note: these tryptic fragments have been ordered by homology with the human sequence
R:Stearne, P.A.; Pietersz, G.A.; Goding, J.W.
J. Immunol. 134, 3474-3479, 1985
A:Title: cDNA cloning of the murine transferrin receptor: Sequence of trans-membrane
A:Reference number: I49662; MUID:85159078; PMID:2984291
A:Accession: I49662
A:Status: translated from GB/EMBL/DBJ

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```

A:Molecule type: mRNA
A:Residues: 'AL',27-149,'Q',151-301 <RES>
A:Cross-references: GB:M29618; NID:9193272; PIDN:AAA37616.1; PID:9193273
C:Comment: This transmembrane glycoprotein exists as a dimer of similar or identical
ty acyl groups. The amino end of each chain lies within the cytoplasm and a stop-tira
embrane, may also serve as an internal signal sequence.
C:Function: The expression of this receptor, involved in the regulation of cell growth
C:Function:
A:Description: mediates cell iron uptake by binding, internalizing, and recycling the
C:Superfamily: transferrin receptor
C:Keywords: glycoprotein; iron transport; receptor; transmembrane protein
F:1-57/Domain: intracellular #status predicted <INT>
F:58-61/Region: stop-transfer sequence
F:62-89/Domain: transmembrane #status predicted <TMS>
F:89-763/Domain: extracellular #status predicted <EXT>
F:101-763/Product: 85K serum transferrin receptor #status predicted <MAT>
F:253,319,730/Binding site: carboxyrate (Asn) (covalent) #status predicted

```

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Query Match      18.7%: Score 435; DB 1: Length 763;
Best Local Similarity 26.7%: Pred. No. 1.5e-24;
Matches 123; Conservative 88; Mismatches 171; Indels 78; Gaps 14;

Oy      1  MGSGAP-----DSWRGSLKSYNVNGPGFTGNFSTQVKMHIHSTNEVRIYVIGTLRG 56

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[illegible]

RESULT 7

UxHU

transferrin receptor - human

N:Alternate names: CD71; p90

N:Contains: 85k serum transferrin receptor

C:Species: Homo sapiens (man)

C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 22-Jun-1999

C:Accession: A93343; A90856; A36597; S54327; S09039; A03259

R:Schneider, C.; Owen, M.J.; Banville, D.; Williams, J.G.

R:Nature 311, 675-678, 1984

A:Title: Primary structure of human transferrin receptor deduced from the mRNA sequence

A:Reference number: A93343; MUID:85012743; PMID:6090955

A:Accession: A93343

A:Molecule type: mRNA

A:Residues: 1-760 <SCH>

A:Cross-references: Kuhn,XO1060; NID:g37432; PIDN:CAA25527.1; PID:g37433

R:McLelland, A.; Ghah, L.C.; Ruddle, F.H.

Cell 39, 267-274, 1984

A:Title: The human transferrin receptor gene: genomic organization, and the complete primary structure

A:Reference number: A90856; MUID:85048936; PMID:6094009

A:Accession: A90856

A:Molecule type: mRNA

A:Residues: 1-760 <MC>

A:Cross-references: MB:ML1507; NID:g339515; PIDN:AAA61153.1; PID:g339516

R:Shih, Y.J.; Baynes, R.D.; Hudson, B.G.; Flowers, C.H.; Skirne, B.S.; Cook, J.D.

J. Biol. Chem. 265, 19077-19081, 1990

A:Title: Serum transferrin receptor is a truncated form of tissue receptor.

A:Reference number: A36597; MUID:91035436; PMID:2229063

A:Accession: A36597

A:Molecule type: protein

A:Residues: 101-103, 'X', 105-108, 'X', 110-119 <SH>

A:Experimental source: serum

R:Coppolino, M.; Migliorini, M.; Argaves, W.S.; Dedhar, S.

Biochem. J. 306, 129-134, 1995

A:Title: Identification of a novel form of the alpha(3) integrin subunit: covalent association with alpha(3) integrin subunit

A:Reference number: S54327; MUID:95169043; PMID:7864799

A:Accession: S54327

A:Molecule type: protein

A:Residues: 288-302,694-708;721-730 <COP>

R:Alvarez, E.; Girones, N.; Davys, R.J.

Biochem. J. 267, 31-35, 1990

A:Title: A point mutation in the cytoplasmic domain of the transferrin receptor inhibits
A:Reference number: S09039; MUID:90226333; PMID:2327986
A:Accession: S09039
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-19, 'C', 21-61 <ALY>
C:Note: mutant defective in endocytosis
C:Comment: This transmembrane glycoprotein exists as a dimer of similar or identical
tyl acyl groups. The amino end of each chain lies within the cytoplasm and a stop-transfer
embrane, may also serve as an internal signal sequence.
C:Comment: The expression of this receptor, involved in the regulation of cell growth.
C:Genetics:
A:Gene: GDB:TFRC
A:Cross-references: GDB:120433; OMIM:190010
A:Map position: 3q26.2-3q26.2
C:Function:
A:Description: mediates cell iron uptake by binding, internalizing, and recycling the
C:Superfamily: transferrin receptor
C:Keywords: glycoprotein, iron transport, receptor, transmembrane protein
F:1-57/Domain: intracellular #status predicted <INT>
F:58-24/Region: tyrosine-based endosomal/Lysosomal sorting signal
F:58-61/Region: stop-transfer sequence
F:62-89/Domain: transmembrane #status predicted <TMS>
F:89-760/Domain: extracellular #status predicted <EXT>
F:101-760/Product: 85k serum transferrin receptor #status predicted <MAY>
F:251,317,727/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 18.3%; Score 426; DB 1; Length 760;
Best Local Similarity 26.5%; Pred. NO. 7.2e-24;
Matches 110; Conservative 94; Mismatches 171; Indels 40; Gaps 11;

OY 31 IQAKYMHSHNEVTRITYNYGTLRGAVERPRRYIILGHRDSWTFGGIDPOSGAAYNHET 90
 Db 370 SKNVKLTIVSNVYLKEIKILINIFGVIKGEVDPHYVYGAQRDMGPRGAKSGVGTALLKLT 429
 OY 91 VRSEGTL-KKEGMEPRRTIIFASMDAEFGLGSGTEMAEDNSRLJOERGVAIYNADSIE 149
 Db 430 AQMSMDVWLKQGPSPRSIIIFASMSADDFGSGVGTATEMTEGLSSLHLKAFYIYLDKAVL 489
 OY 150 GNYLRVDCPIPLAMISLYNLTLEKLSPEDEGEKSLYE--SWTKSSPERSGMPRI SKL 207
 Db 490 GTSNFKVASASLVTLEKTQMNVKHPR--VTGGFLYODSNWASK-----VEKL 535
 OY 208 GSGNDPEFEFQRLGLASGRARYTKNMETNKSGPILVSHSYEY-ELVEKPYDPMFKYHL 266
 Db 536 TLDMAAPPELAYSISIPAVSFCECED-----TDVPIGLTMDTYKLELIERPE-LNKVAR 588
 OY 267 TVAOVRGGMPEFLANSIYLPDPCRDYAVLYRKYADKIYINISMKRPQEMKIYLSLFSDSLFS 326
 Db 589 AAAYEAOFYKTLHVDVDELINLDYERYNSQLSFPYRDL---NQRADIKEMGSLSLQWLYLS 644
 OY 327 AVKNETELASKEFSERLDDFKSNPILLRMMNDQMLFERAFIDPLGLPDRFRYRHVIYAP 386
 Db 645 ARGGEFPAISLTLTDFGNAEKTDRFYVKKLLDRMRYREYHPLSLYVSPKESPRFHYWGS 704
 OY 387 SSNNKYAGESPPGIYDALFDIESKYVDPSKAMGV--KRQISVAFTYQAAAETLS 439
 Db 705 GSH-----TLPAL--LENLKLKRNQNGAFNETLFRQNALATLATWITQGANMALS 750

RESULT 8
 A48592
 transferrin receptor protein - Chinese hamster
 C:Species: Citicellus griseus (Chinese hamster)
 C:Date: 03-May-1994 #sequence.revision 03-May-1994 #text.change 20-Aug-1999
 C:Accession: A48592
 R:Collawn, J.F.; Lai, A.; Domingo, D.; Fitch, M.; Hutton, S.; Trowbridge, I.S.
 J. Biol. Chem. 268, 21682-21692, 1993
 A:Title: yvrf is the conserved internalisation signal of the transferrin receptor, an
 A:Reference number: A48592; MUID:94012749; PMID:8408022
 A:Accession: A48592
 A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-757 <COL>
 A:Cross-references: GB:LI9142; NID:g304528; PION:AAA03576.1; PID:g304529
 C:Superfamily: transferrin receptor
 C:Keywords: endocytosis; glycoprotein; transmembrane protein

Query Match 18.2%; Score 424.5; DB 2; Length 757;
 Best Local Similarity 24.9%; Pred. No. 9.3e-24;

Matches 114; Conservative 88; Mismatches 182; Indels 73; Gaps 11;

1 MGSGAPDDSSWRGSLKSYNVNPGFTGNFSTQKVMHISTNEVTRIVNIGTLRGAVEP 60
 Db METNCP--SMNDSJCKLESQGINVLS-----VNNVLAKEFRLNIFGVYIKGEEP 396
 QY 61 DRYVILIGHRDSVFEIGIDPQSCAAVYHETVRSFGL-KKEGMRPRTTILFASWDAEEFG 119
 Db 397 DRIYVAGADRDAGPAAKSSVGTGLLKLQAFSDMVSRGFGKPSRSITFASMSAGDFG 456
 QY 120 LIGSTMAEDNSRLDERGAVYINADSSIEGNTLVDCPLKYSLVYNLTRELKSPDEG 179
 Db 457 AVGATMELGYSLSLHKAFETYINLDKVVYGTNFKVYASPLLYTILEKTMOVRP-- 513
 QY 180 FEKSLY-ESWTK-----SPSEFGMPRIKLSGNDPEVEFQRLGIASGRA 227
 Db 514 IDGKPLYRDSNMWISKVEDSLDAAAPFLAYSGIPAVSFECNE----- 558
 QY 228 RTKKNMETHKFSYPLVSHVYETELVEKFDYDMERYHLTVAGVRCGMVFEANSLVLPF 287
 Db 559 -----DYPYLDINLDYTEKLIQKVPOLNMKVRNAAEVAQOIFIKLTHDIELNL 606
 QY 288 DCRDYAVLRKYADKLYINISMKHPQ---EMKTYSLSPDSLFSKVNKPTETLASFSERLD 344
 Db 607 D-----YDMYNNKILSFYKELNDFRADIKAMGSLQWLYSARGDFRATSLTDFPHN 659
 QY 345 FPKSNPILIRMMNDQMLERAFIDPLDRPFYRVHYIAPSSHNKYAGESPFIYDAL 404
 Db 660 AAKTNFVYREINNRIMKVEYHPLSPYSPRSPEFHIMGSSSHLTA-----LV 710
 QY 405 FDIKSVKDSKAMGDV--KRQISVAFTVQAAAEITLS 439
 Db 711 ENLKLRQKNSSAFNETLFRNOLATWTIQVANAMLS 747

RESULT 9

JH0570
 transferrin receptor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JH0570; S16855
 R:Gerhardt, E.M.; Chan, L.N.L.; Jing, S.; Qi, M.; Trowbridge, I.S.
 Gene 102, 249-254, 1991
 A:Title: The cDNA sequence and primary structure of the chicken transferrin receptor.
 A:Reference number: JH0570; MUID:91340160; PMID:1874449
 A:Accession: JH0570
 A:Molecule type: mRNA
 A:Residues: 1-776 <GER>
 A:Cross-references: EMBL:X55348
 A:Note: 581-His and 736-Gln were also found as the result of polymorphism
 C:Comment: This protein mediates the endocytosis of the iron transferrin complex.
 C:Superfamily: transferrin receptor
 C:Keywords: glycoprotein; lipoprotein; phosphoprotein; receptor; thiolester bond; transmembrane; coated-pit mediated internalization signal
 F:19-22/Region: coated-pit mediated internalization signal
 F:70-88/Domain: transmembrane #status predicted <TRK>
 F:23/Binding site: phosphate (Ser) (covalent) #status predicted
 F:70/Binding site: palmitate (Cys) (covalent) #status predicted
 F:261,326,391,738/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.8%; Score 413.5; DB 1; Length 776;
 Best Local Similarity 27.1%; Pred. No. 6.5e-23;

Matches 121; Conservative 84; Mismatches 175; Indels 67; Gaps 14;

QY 11 WRG---SLKSYNVNPGFTGNFSTQKVMHISTNEVTRIVNIGTLRGAVEPDRYVILG 67
 Db 367 WKGAHSCQV-----TKHESQIMVRLDVNNSMKDKRIINICGAIQGFEPDRYVIG 419

QY 68 GHRDSWFEIGIDPQSCAAVYHETVRSFGL-KKEGMRPRTTILFASWDAEEFGLGSGTEW 126
 Db 420 AQRDSWEPGAKKAGTGTAILELARVSDLYKNGYPRRSITIFASMSAGDYGAVGATEW 479

QY 127 AEDNSRLDERGAVYINADSSIEGNTLVDCPLKYSLVYNLTRELKSPDEGFEKSLY 186
 Db 480 LEGYSAMLHAKAFETYISLDAPVLGASHVKISASPLLYNLGSIIMKGVKNP--AAVSSSLY 537

QY 187 E-----SWTK-----KSPSEFGMPRIKLSGNDPEVEFQRLGIASGRARTKN 232
 Db 538 NRIQPDWYKAVVPLDGLDAAAPFLAYSGIPVLS-----FGRY----- 574

QY 233 WETNKFSGYPLVSHVYETELVEKFDYDMERYHLTVAGVRCGMVFEANSLVLPFCRCRY 292
 Db 575 ---NKDEYFEDTKGDTLENLKRIT-DNLDAALAAAEVAGQALRLTHDHELPLDIGRY 630

QY 293 AVVLRKYADKLYINISMKHPQEMKTYSLSPDSLFSKVNKPTETLASFSERLDPEKSNPL 352
 Db 631 SEELLAYQEEF---LPYIKVEYRELGLTLDLPPFAGDPQRAVTALRDIANDSGENRY 686

QY 353 LRMMNDQMLERAFIDP-LGLPDRPFYRVHYIAPSSHNKYAGESPFIYDALFDIESKY 411
 Db 687 RRALNDRMKKVEYDFLSPYLPKDVPE-RIIFPGKGPHTL---RSIVHLLQLTKTRNSVY 742

QY 412 DPKAMGDVYKQISVAFTVQAAAEITL 438
 Db 743 DNLN-----LREQALATWTIQVANAMLS 765

RESULT 10

S57149
 Probable membrane protein YJR126c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein J2050
 C:Species: Saccharomyces cerevisiae
 C:Date: 23-Aug-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002
 C:Accession: S57149
 R:Rose, M.; Koetter, P.; Entlian, K.D.
 Submitted to the Protein Sequence Database, September 1995
 A:Reference number: S56848
 A:Accession: S57149
 A:Molecule type: DNA
 A:Residues: 1-811 <ROS>
 A:Cross-references: EMBL:Z49626; NID:g1015854; PID:g1015855; GSPDB:GN00010; MIPS:YJR1
 C:Genetics:
 A:Gene: MIPS:YJR126c
 A:Cross-references: SGD:S0003887
 A:Map position: 10R
 C:Keywords: transmembrane protein

Query Match 17.1%; Score 399; DB 2; Length 811;
 Best Local Similarity 27.5%; Pred. No. 8.4e-22;

Matches 119; Conservative 77; Mismatches 164; Indels 72; Gaps 15;

QY 19 YNVGPG-----FTG-NFSTQKVMHISTNEVTRIVNIGTLRGAVEPDRYVILGCH 69
 Db 387 FQIGPNSNIKDRGSPGSSIDKXVHNLNLYNKEMSSVAVSLPG-IFTEGELLIGAH 445

QY 70 RDSWVFGGL-DPQSCAAVYHETVRSFGLKKEGMRPRTTILFASWDAEEFGLGSGTEMAE 128
 Db 446 RSLSSSSAGANSASALLEIARQMSKILKHGMPLRPIKILSDWGERSGSLSTVAE 505

QY 129 DNSRLDERGAVYINADSSIEGNTLVDCPLKYSLVYNLTRELKSPDEGFEKSLY 188
 Db 506 AHAALTRRALVYLMDNAISGT-NFCKKANDLDVDVYEAAK--LTERNGHEDWSLEDDH 562

QY 189 WTKKSPSEFGMPRIKLSGNDPEVEFQRLGIASGRARTKNMETHKFSGYPLVH--SS 246
 Db 563 W-----KYSNATISLIDGLSVTSFYHGLGVPAHFGF-----NANDTSG-AVYHNS 610
 QY 247 VYETELVEKFDYDMERYHLTVAGVRCGMVFEANSLVLPFCRCRYAVVLRKYADKTY-- 304
 Db 611 VFDSPTWLEKFTNSDYKLNHTWAMFVGLTTLMLSENELARFN-----THVYLLKRIYNW 663

305 -----NISMKHQEMKTYSLSPDSLSAVKNFETLAKSFERSLQDPDKSNPIL----- 352
664 YIAWHSNLSAFAPODDV-----NSLAKRYDLKVAFO--EDSIQDQNGILYKRCRE 716
353 -----LRMNDQLMFLERAFIDPLGPDREYRHHVYADSSHNKIYGES 396
717 ALPWAAFYKKIKYIKIQRNSKSKQIDQLFTHRGKLDREMMKYSLLAPSKFEGSVGEV 776
397 FPGIYDALFDIE 408
777 LFGIHEGLADID 788

RESULT 11

40289
hypochemical protein SPBC354.09c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: T40289
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hildbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, March 1998
A:Reference number: 221918
A:Accession: T40289
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-794 <MOO>
A:Cross-references: EMBL:AL022071; PIDN:CAA17809.1; GSPDB:GN00067; SPDB:SPBC354.09c
A:Experimental source: strain 972h-; cosmid c354
C:Genetics:
A:Gene: SPDB:SPBC354.09c
A:Map position: 2
C:Superfamily: secretory protein SSP134

Query Match 15.2%; Score 355; DB 2; Length 794;
Best Local Similarity 25.0%; Pred. No. 1.6e-18;
Matches 105; Conservative 80; Mismatches 185; Indels 50; Gaps 13;

11 WRGSLKSYNVGFGFPGNFSTQKVKHISTNEVTRVYVIGTLRGAVEDPRVYILGHR 70
402 WTGS-KIS--SPGLEVN-----LQDIEKQKTIINMAQIDG-YESDQLLVGAPR 448
71 DSWVFGIDPQSGAAYVHETVRSFGLTKE-GMRPRRTILFASWDAEFGILGSTEAE 129
449 DSWCTGSDSVGTSLIDVISTFANNAQDLSMKPRRTIYFASMDARQFMAIGSTEFLEY 508
130 NSRLQERGVAIYNADSSIEGNTLRYDCYPLMTSLVYNLTKEKSDDEGEKSLYESW 189
509 WKSELEKAVAIYIVDAVAGSD-TFTARTVPGLEKVIQRAFDVANEDEMKANITDDF 567
190 TKKSPSPFSGMPRIKSLGSGNDEVFQORGLASGRARYTKNMTNKGSGYPLHYSYE 249
568 DYTGS-----DLTSFLTFAGIPIVYNLAFTERNEPN--TTPFLGSCED 607
250 TYELVEKFDPMFYHLTVAVQRGVAFELANSIVLPFCRDYAVVLRKYADKIYNISMK 309
608 TVSWIDTFGESEYWEAALGKIMSYLLIFLAMPVPPVLDLEDEINGVEMLKRIPEIGA 667
310 HPOEKRTYSLSPDSLSFAVKNFETLAKSFERSLQDPD-----KSNPILLRMNDQLMFL 364
668 NALDARKNEESSELLESLIRFEDEIRMKSLIMHNSYTVSVKHP-ELEGYNALARFE 726
365 RAFIDPLGIDPRPRYRHHVYADSSHNKKAAGESFPGIYALF--DIESKVDPSKANGDYKR 422
727 RSFLDEAGLPGHEWYKHLIYGPNLRNHS-QLFSPSLDALYGDVEA-----AQKEVVR 779

RESULT 12
E85075
probable peptidase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: E85075

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: E85075
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-280 <STO>
A:Cross-references: GB:NC_001268; NID:97267364; PIDN:CAB81137.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g07670
A:Map position: 4

Query Match 10.8%; Score 252; DB 2; Length 280;
Best Local Similarity 45.5%; Pred. No. 1.9e-11;
Matches 51; Conservative 16; Mismatches 27; Indels 18; Gaps 3;

20 NVGPFGTFNSTQKVKHISTNEVTRVYVIGTLRGAVEDPRVYILGHRDQWVFGID 79
147 DVGPG-PGILNLSYL-----VTKIQNVIGVIEGEEEDPRVYILRNHRDTWTFRAVD 196
80 PQSGAAYVHETVRSF-----GTLKEGMRPRRTILFASWDAEFGILGS 123
197 PMSGTAIVLMEASKSYLQHTAQRDLQKRGKMPKRTIILCNDADEYGLVSS 248

RESULT 13

567153
probable membrane protein YOR256c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O5330
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
R:Jauniaux, J.C.; Poirey, R.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67143
A:Accession: S67153
A:Molecule type: DNA
A:Residues: 1-809 <JAU>
A:Cross-references: EMBL:Z75164; NID:91420578; PIDN:CAA99478.1; PID:91420579; GSPDB:G
A:Experimental source: strain S288C
C:Genetics:
A:Gene: MIPS:YOR256c
A:Cross-references: SGD:S0005782
A:Map position: 15R
C:Superfamily: secretory protein SSP134
C:Keywords: transmembrane protein
F:126-142/Domain: transmembrane #status predicted <TM>

Query Match 10.3%; Score 240.5; DB 2; Length 809;
Best Local Similarity 22.4%; Pred. No. 6.4e-10;
Matches 98; Conservative 78; Mismatches 160; Indels 101; Gaps 19;

47 IYVNIIGTLRGAVEDPRVYILGHRDQWVFGIDPQSGAAYVHETVRSFGLTKEGMRPR 105
423 IPNIYKIEGREGOSKALIIAASRNSINFGTYPFAGTALLISTYQLFOEKYKFGMKPL 482
106 RTILFASWDAEFGILGSTEAEEDNSRLQER-----GVAYINADSSIEGNTYLR 155
483 RNIVPISFGGEFNFYAGSSELYEQRLTPLKDEIYSLIDISQIGIFAKYENGKRGELS 542
156 VDCTPLMYSLVYNLTKEKSDDEGEKSLYESWTKKSPSPF-SGMRISKLSGNGNFE 214
543 IETHPLLKFF-FNRNAH-GNFDISVDNVQHYGDWF-----PFLANGIP-VSVYSSD---- 590
215 VFQORGLASGRARYTKNMTNKGSGYPLHYSVETIYELVEKFYDP-----MFK 263
591 -----STRNRDPT-ETSE-----DKFERVERILEDEONQSVKDLVYL 629
264 YHITVAQVAGVAFELANSIVLPFCRDYAVVLRKYADKIYNISMKHQEMKTYSLSPDS 323
630 LHISM-----ELIDPLLFHFDIIST--VEDIDERLQLEQAVYPERK-----LNFTS 672

```
OY 324 LFSAVKNTETIASKFSERLQDF-----DKSNPILLRM---MNDQMLFERAFIDPL 371
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 673 IKGLLEFMKKISEMAWMTQGMENIYWSHGDIPELISINRWTKKRLTINIGRITCSPA 732
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 372 GIPDRPFYHYHYAAS-----SHNKYAGE-----SFPCTIYALDIESKVPSPKAMGVKQ 423
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 733 GLPNRSFYKNVLFGLPTLLQEDKSKNGNVDFTFPGVDATYDD-----WKRAQEQ 784
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 424 ISVAAFVQAAAEFLSE 440
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 765 IDLIGKVLHQSAALFVE 801

RESULT 14
S65188
secretory protein SSP134 - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein P2267; protein YPL176c
C:Species: Saccharomyces cerevisiae
C>Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 19-Apr-2002
C:Accession: S65188; JH0485
R:Benes, V.; Rechmann, S.; Nentwich, U.; Voss, H.; Ansorge, W.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S65183
A:Accession: S65188
A:Molecule type: DNA
A:Residues: 1-783 <BEN>
A:Cross-references: EMBL:Z73532; NID:q1370370; PIDN:CAA97883.1; PID:q1370371; MIPS:YPL17
A:Experimental source: strain S288C (A9972)
R:Sidhu, R.S.; Mathewes, S.; Bolton, A.P.
Gene 107, 111-118, 1991
A:Title: Selection of yeast protein-encoding genes by fusion with PHO5 in Saccharomy
A:Reference number: JH0483; MUID:92077420; PMID:1743509
A:Accession: JH0485
A:Molecule type: DNA
A:Residues: 66-149, 'P', 151-318, 'R', 320-414 <SID>
A:Note: the authors claim that sequence of residues 41-57 is signal sequence
A:Note: the authors translated the codon TTA for residue 34 as Phe, GAT for residue 201
C:Genetics:
A:Gene: SSP134
A:Cross-references: SGD:S0006097
A:Map position: 16L
C:Superfamily: secretory protein SSP134
C:Keywords: glycoprotein
F:139, 213/Blinding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.7%; Score 179.5; DB 2; Length 783;
Best Local Similarity 19.7%; Pred. No. 2.3e-05;
Matches 93; Conservative 82; Mismatches 169; Indels 127; Gaps 20;

OY 15 LKSYNVGPGFTGNFSTOKVKMHIST-NEVTRIVYIGTLRGAVPEPDRYVILGGHRDM 73
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 374 VAFSNNL---FSGSLNDCKLIDLIVQTAIEKRPVHDIVKIEGSEDAQAIVIAAFRNSA 430
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 74 VEGGIDPOSGAAVHETVRSFGLT-KKEGMRPRRTILFASMDAEFGLLGSTEWADNSR 132
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 431 SYGTWPSFGYVVLISLLQYQEMVKKFPMKPLRNIFYISFGSEFENAGATEIMEKRE 490
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 133 LQERGVAAIYNA-----DSSIEGNYTLRVCTPLMISLVNLTRELKSPDEGFGSKL 185
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 491 ALKSEIYTIIDVGQIGIMDSN---NLEIOCHPLVDL---FOKNMRSRKNVAVDV 542
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 186 YE-SWTKKSPPEFS-GMP--RISKLISGNDFEVFF---ORLGISGARATYKNETNK 237
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 543 HQPGDMT-----PYLAQGIPIVALISPGVMNREHPYIYEDKFDPLKDLRKKGCEV-- 595
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 238 FSGYPLYSVSYETVELVEKFDPMKRYHLTVAQVRCGMAVEFLANSIVLPDCRDYAVLR 297
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 596 LSEIMLY-----LVKK-----SLELIDPEIFPFSISNYDFL- 627
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 298 KYADKIYNSMKHPQEMKTYISLSPDSLFSAVKNFTETIASKFSERLQDFPKSNPILRRMN 357
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 628 -----STTLKDLQKCPDVIYNFDEVFLGTTIMENTKLQFEKMSW----- 668
```

```
OY 358 DQMLFERAFIDPL-----GLPDRPFYHYHYAASSHNKYA 393
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 669 TELMWACGYIEPTTIAINRMSWNVLLSLIGVQCLEGIMDRTEFKNVIFGKLM----- 724
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 394 GESFPGIYALDIESKVPSPKAM--GDYKROIYNAAF-TVQAAATLSEV 441
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 725 -----VDKGPLRSWTFPEIRDTIADKMSVSVOQAWTLGTI 761
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
G82759
hypothetical protein XF0820 (imported) - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
C:Accession: G82759
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: G82759
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <SIM>
A:Cross-references: GB:AE003921; GB:AE003849; NID:g9105710; PIDN:AAF83630.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Birones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre
as-Neito, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshahov, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0820
C:Superfamily: Xylella fastidiosa hypothetical protein XF0820

Query Match 7.4%; Score 173; DB 2; Length 529;
Best Local Similarity 31.1%; Pred. No. 4e-05;
Matches 66; Conservative 30; Mismatches 70; Indels 46; Gaps 11;

OY 42 NEVTRIVYIGTLRGAVPEPDRYVILGGHRD-----SWVF-GGIDPOSGAAVHE 89
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 270 SEVITSHNVAARLOGCAHDEVIYISAHMDHLCVGAPDAKGDITFPGALDMSGTAALE 329
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 90 TVRSFGLTKEGMRPRRTILFASMDAEFGLLGSTEWADNSRLQERGVAYINAD---- 145
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 330 LARGFA-----RGQPORSVLFVLAETAEKGLIGS--EYVASNPILYPERKIVAAVINMOMVNP 384
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 146 -----SSIEGNY-TLRVCTPLM-----YSLVYNLTRELKSPDEGFGSKLSYSWTKKSPS 195
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 385 QGFTRDGFIYGTAKDLLDLMLKOVAAAGMKRLRYLD--PTEAGHFRNSDHFSAFR--- 438
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 196 PEFSGMRISKLISGNDFEVFFQRLGIASGRA 227
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 439 -----GIPALS-YSAQGDMEVG-----GYAAGKA 461
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: October 4, 2003, 23:26:01
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2003, 23:00:27 : Search time 77 Seconds
(without alignments)
1481.289 Million cell updates/sec

Title: US-09-973-382C-2
Perfect score: 2329
Sequence: 1 MGSAPDPSWRGSLKVSYN.....QISVAFTVQAALTLSEVA 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2329	100.0	442	4 Q9HBA9	Q9HBA9 homo sapien
2	2097.5	90.1	719	4 Q8TAY3	Q8TAY3 homo sapien
3	571.5	24.5	614	16 Q8PGK5	Q8PGK5 xanthomonas
4	545.5	23.4	1483	5 Q93J32	Q93J32 caenorhabdit
5	415.5	17.8	768	6 Q8H2V3	Q8H2V3 sus scrofa
6	412	17.7	621	10 Q94JH4	Q94JH4 oryza sativ
7	404.5	17.4	298	10 Q8LQ61	Q8LQ61 oryza sativ
8	353.5	13.2	606	10 Q94JH3	Q94JH3 oryza sativ
9	252	10.8	280	10 Q9XH28	Q9XH28 arabidopsis
10	240.5	10.3	809	3 Q08693	Q08693 saccharomyc
11	224.5	9.6	515	11 Q08872	Q08872 mus musculu
12	179.5	7.7	783	3 Q08919	Q08919 saccharomyc
13	173	7.4	529	16 Q09PF58	Q09PF58 xylella fas
14	158	6.8	549	16 Q8P530	Q8P530 xanthomonas
15	157	6.7	467	16 Q9A5A8	Q9A5A8 caulobacter
16	156	6.7	549	16 Q8PP50	Q8PP50 xanthomonas

17	152.5	6.5	430	16 Q9A3U5	Q9A3U5 caulobacter
18	151	6.5	514	16 Q8EBH7	Q8EBH7 shewanella
19	149	6.4	501	2 P96152	P96152 vibrio chol
20	148	6.4	501	16 Q9KID3	Q9KID3 vibrio chol
21	146.5	6.3	375	16 Q8P625	Q8P625 xanthomonas
22	146.5	6.3	536	16 Q8P326	Q8P326 xanthomonas
23	144.5	6.2	449	2 Q93EJ5	Q93EJ5 bacillus 11
24	142.5	6.1	472	16 Q8PHE8	Q8PHE8 xanthomonas
25	139.5	6.0	393	2 Q82996	Q82996 aeromonas p
26	138	5.9	1066	16 Q8CK35	Q8CK35 streptomyce
27	137.5	5.9	337	17 Q8TY04	Q8TY04 methanopyru
28	136	5.8	470	11 Q9WVJ3	Q9WVJ3 mus musculu
29	133.5	5.7	536	16 Q8PFH7	Q8PFH7 xanthomonas
30	133	5.7	374	3 Q04033	Q04033 saccharomyc
31	131	5.6	472	11 Q91IV0	Q91IV0 rattus norv
32	131	5.6	472	11 Q921Y1	Q921Y1 rattus norv
33	130.5	5.6	500	16 P96264	P96264 mycobacteri
34	128.5	5.5	522	16 Q8ED13	Q8ED13 shewanella
35	126.5	5.4	493	5 Q76552	Q76552 acanthocheil
36	126	5.4	485	2 Q53737	Q53737 streptomyce
37	122.5	5.3	472	4 Q8NB21	Q8NB21 homo sapien
38	122.5	5.3	472	4 Q9T646	Q9T646 homo sapien
39	122.5	5.3	541	4 Q9Y5X6	Q9Y5X6 homo sapien
40	121.5	5.2	536	16 Q9HZ08	Q9HZ08 pseudomonas
41	121	5.2	598	16 Q8PRD7	Q8PRD7 xanthomonas
42	120.5	5.2	324	16 Q9F2X2	Q9F2X2 streptomyce
43	120	5.2	506	16 Q8EP07	Q8EP07 shewanella
44	120	5.2	594	16 Q8PER6	Q8PER6 xanthomonas
45	117	5.0	609	2 Q8VUS4	Q8VUS4 alteromonas

ALIGNMENTS

RESULT 1
Q9HBA9 PRELIMINARY; PRT; 442 AA.
AC Q9HBA9:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DT Prostate-specific membrane antigen-like protein.
GN PSMA/SCP III.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA O'Keefe D.S., Bacich D.J., Heston W.D.W.;
RT "Expression Profile of Prostate-Specific Membrane Antigen (PSMA)
RT versus a Prostate-Specific Membrane Antigen-Like Gene in Normal
RT Tissues, Prostate Cancer and Tumor Associated-Vasculature."
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA O'Keefe D.S., Bacich D.J., Heston W.D.W.;
RT "Cloning and Characterization of a novel glutamate-preferring
RT peptidase that maps to the SCZDI1 locus: a candidate gene for
RT schizophrenia".
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF261715; AAG29102.1;
DR Pflam; PF04253; TFR_dimer; 1.
SQ SEQUENCE 442 AA; 50044 MW; 26CD6E082AC1B8D3 CRC64;

Query Match 100.0%; Score 2329; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.6e-170;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSAPDPSWRGSLKVSYNPGFTGNFSTQKVKMHISTNEVRIINVIGTLGAVEP 60
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Db 1 MGSAAPPDSSMRGSLKSYNVNGPGFTGNFSTQKYKMHISTNEVTRIVNIGTLRGAVEP 60
QY 61 DRYVILGGHRDSWFGGIDPQSGAAVYHETVRSFGLTKEGMRPRRTILFASMDAEFGL 120
Db 61 DRYVILGGHRDSWFGGIDPQSGAAVYHETVRSFGLTKEGMRPRRTILFASMDAEFGL 120
QY 121 LGSTEMADNRRLLQERVAIYNADSSIEGNYTLRVCTPLMYSLVNLTLEKSPDEGF 180
Db 121 LGSTEMADNRRLLQERVAIYNADSSIEGNYTLRVCTPLMYSLVNLTLEKSPDEGF 180
QY 121 LGSTEMADNRRLLQERVAIYNADSSIEGNYTLRVCTPLMYSLVNLTLEKSPDEGF 180
Db 121 LGSTEMADNRRLLQERVAIYNADSSIEGNYTLRVCTPLMYSLVNLTLEKSPDEGF 180
QY 181 ECKSLYESWTKKSPSPESGMPRISKLSGNDPEFFFORLGIASGRARYTKNMTNKFSG 240
Db 181 ECKSLYESWTKKSPSPESGMPRISKLSGNDPEFFFORLGIASGRARYTKNMTNKFSG 240
QY 181 ECKSLYESWTKKSPSPESGMPRISKLSGNDPEFFFORLGIASGRARYTKNMTNKFSG 240
Db 181 ECKSLYESWTKKSPSPESGMPRISKLSGNDPEFFFORLGIASGRARYTKNMTNKFSG 240
QY 241 YPLXHSYETVELVEKPYDPMFKYHLTVAAQYRGGMVELANSIYLPDPCRDYAVVLRKYA 300
Db 241 YPLXHSYETVELVEKPYDPMFKYHLTVAAQYRGGMVELANSIYLPDPCRDYAVVLRKYA 300
QY 301 DKITNISKHPOEKKTYSLSFSDSLFSAVKNTETLASKFSERLQDFDKSNPILLRMNDOL 360
Db 301 DKITNISKHPOEKKTYSLSFSDSLFSAVKNTETLASKFSERLQDFDKSNPILLRMNDOL 360
QY 301 DKITNISKHPOEKKTYSLSFSDSLFSAVKNTETLASKFSERLQDFDKSNPILLRMNDOL 360
Db 301 DKITNISKHPOEKKTYSLSFSDSLFSAVKNTETLASKFSERLQDFDKSNPILLRMNDOL 360
QY 361 MFLERAFIDPLGLDPRPYRHVITYAPSSHNKYAGESEFPGIYDALFDIESKYDPSKANGDV 420
Db 361 MFLERAFIDPLGLDPRPYRHVITYAPSSHNKYAGESEFPGIYDALFDIESKYDPSKANGDV 420
QY 421 KRQISVAAFVQAAAEFTLSEVA 442
Db 421 KRQISVAAFVQAAAEFTLSEVA 442
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RESULT 2

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OC 08TAY3 PRELIMINARY; PRT: 719 AA.
AC 08TAY3:
DT 01-JUN-2002 (Tremblrel. 21, Created).
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Similar to folate hydrolase (Prostate-specific membrane antigen)
DS 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC025672; AAB25672.1; -.
DR InterPro; IPR003137; PA.
DR Pfam; PF02225; PA; 1.
DR Pfam; PF04253; TFR_dimer; 1.
DR PROSITE; PSS0840; PA; 1.
KW Hydrolase.
SQ SEQUENCE 719 AA; 80597 MW; AF79A10CA2BF9DP4 CRC64;
```

Query Match 90.1%; Score 2097.5; DB 4; Length 719;
Best Local Similarity 91.0%; Pred. No. 1.9e-152;
Matches 402; Conservative 6; Mismatches 3; Indels 31; Gaps 1;

```
QY 1 MGSAAPPDSSMRGSLKSYNVNGPGFTGNFSTQKYKMHISTNEVTRIVNIGTLRGAVEP 60
Db 309 MGSAAPPDSSMRGSLKSYNVNGPGFTGNFSTQKYKMHISTNEVTRIVNIGTLRGAVEP 368
QY 61 DRYVILGGHRDSWFGGIDPQSGAAVYHETVRSFGLTKEGMRPRRTILFASMDAEFGL 120
Db 369 DRYVILGGHRDSWFGGIDPQSGAAVYHETVRSFGLTKEGMRPRRTILFASMDAEFGL 428
QY 121 LGSTEMADNRRLLQERVAIYNADSSIEGNYTLRVCTPLMYSLVNLTLEKSPDEGF 180
Db 429 LGSTEMADNRRLLQERVAIYNADSSIEGNYTLRVCTPLMYSLVNLTLEKSPDEGF 488
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QY 181 ECKSLYESWTKKSPSPESGMPRISKLSGNDPEFFFORLGIASGRARYTKNMTNKFSG 240
Db 489 ECKSLYESWTKKSPSPESGMPRISKLSGNDPEFFFORLGIASGRARYTKNMTNKFSG 548
QY 241 YPLXHSYETVELVEKPYDPMFKYHLTVAAQYRGGMVELANSIYLPDPCRDYAVVLRKYA 300
Db 549 YPLXHSYETVELVEKPYDPMFKYHLTVAAQYRGGMVELANSIYLPDPCRDYAVVLRKYA 608
QY 301 DKITNISKHPOEKKTYSLSFSDSLFSAVKNTETLASKFSERLQDFDKSNPILLRMNDOL 360
Db 609 DKITNISKHPOEKKTYSLSFSDSLFSAVKNTETLASKFSERLQDFDKSNPILLRMNDOL 656
QY 361 MFLERAFIDPLGLDPRPYRHVITYAPSSHNKYAGESEFPGIYDALFDIESKYDPSKANGDV 420
Db 657 -----KHVITYAPSSHNKYAGESEFPGIYDALFDIESKYDPSKANGDV 697
QY 421 KRQISVAAFVQAAAEFTLSEVA 442
Db 698 KRQISVAAFVQAAAEFTLSEVA 719
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RESULT 3

```
OC 08PGK5 PRELIMINARY; PRT: 614 AA.
AC 08PGK5:
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Peptidase.
GN XAC3611.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Queglio R.B., Montecro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Camvan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Ciarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Queglio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A.F., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012011; AAM38454.1; -.
DR Pfam; PF04253; TFR_dimer; 1.
KW Complete proteome.
SQ SEQUENCE 614 AA; 66255 MW; 636C3FE15BF00BDD CRC64;
```

Query Match 24.5%; Score 571.5; DB 16; Length 614;
Best Local Similarity 30.5%; Pred. No. 2.3e-35;
Matches 148; Conservative 78; Mismatches 176; Indels 83; Gaps 13;

```
QY 1 MGSAAPPDSSMRGSLKSYNVNGPGFTGNFSTQKYKMHISTNE-VTRIVNIGTLRGAV 58
Db 145 LGGVAPD-DWRGALPTTYRIG-----GDARARVHLKVDADWGSGQTIVNATTLKGE 196
QY 59 EPDRYVILGGHRDSWFGGIDPQSGAAVYHETVRSFGLTKEGMRPRRTILFASMDAEF 118
Db 197 YPDQWVYRGHNRDQWVGADADPLSGTALLAEAKAIGELAKGQORPARKTIVYASMDGEA 256
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[illegible]

ID	093332	PRELIMINARY;	PRT: 1483 AA.
AC	093332:		
DT	01-FEB-1997 (TREMBLrel. 02, Created)		
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	C35C5.2 protein.		
GN	C35C5.2.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;		
OC	Rhabditidae; Pelodierinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	White S.;		
RL	Submitted (Aug-1996) to the EMBL/Genbank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99069613; Pubmed=9851916;		
RA	none;		
RT	"Genome sequence of the nematode C.elegans: A platform for		
RT	investigating biology."		
RL	Science 283:2012-2018(1998).		
DR	EMBL: 278417; CAB01688.1;		
DR	MORPES: M28.011;		
DR	MORPRep: C35C5.2; CE08584.		
DR	InterPro: IPR003137; PA.		
DR	Pfam: PF02225; PA. 2.		
DR	Pfam: PF04253; TFR_dimer; 2.		
DR	PROSITE: PS50840; PA. 2.		
SO	SEQUENCE 1483 AA; 168164 MW; AE07537AD85E8FPC CRC64;		
Query Match	23.4%;	Score 545.5;	DB 5; Length 1483;
Best Local Similarity	31.1%;	Pred. No. 8.5e-33;	
Matches 147;	Conservative 84;	Mismatches 181;	Indels 61; Gaps 16
QY	1 MGSAAPDPSWVSGSLKVSXINVGPRGTGNSTQKVNKHINSTN-----V 44		
DB	320 MKGDA-VNADFGKLVNTVYRGRLINN---OKRLVTYHAENDEKRSVIYVELISRLNLF 375		
QY	45 TRIVNVIGTLRGAVRPRRVYILGHNDSVFGGIDRPSGAAVYVHETVRSFGTLKKE-GWR 103		
DB	376 RLIQNIIMGTLKISQSPDKFVLVSNHYDAWTYGAUVDPSNSTLLEYSRALKQYONOTGM 435		

Oy	104	RRRTLTYSWAAEEGLIGSTEMADNSRLTQBRGAAYINAASSIEGNTLRVDCSPHXY	163
Dd	436	PARSILTFHHMDIEBGLIGSTEFABEYRIQLMRRAVAATNMD-LIGNGOTLLGSNPYA	494
Oy	164	SLUYMLTRELKSPD--EGFEG-KSLYESWTKKPSPEFGSMRISKL-OSGNDFEVFQR	219
Dd	495	NVLRSAAANVEDPNTTEMGGRKTLTDLSMKYYAPSKNNNSTHPYQALIPAGSDSHLPFDY	554
Oy	220	LGI-----ASGARATYKNMETNFESGYPLXHSYIETYLEVEKEFYDPMEKHYLITVAQVR	272
Dd	555	LGIPIVFETTSLDAPPT-----YPLVHTIETEPYLLEINIMDPGVKYKAITAGMF	604
Oy	273	GGWFELANSYLVPRDCRDYAVVLYLKADKIYNISKNHQEM-KITYSL--SEDSLSFSAYK	329
Dd	605	IECIIKTFTESKLIPLYDLNEL-----MDDSIIEFYPEKLEDRIKNTLMIGTKTYDLLDAOK	658
Oy	330	NPTELASKFSESLDOFOFSN-----PLLMM-NMDOCLMFLERAFIDDLGLPDRPFYRH	381
Dd	659	QFKLQKTAVLEISEIVQRNNVSKLEEPLPGSRVDVINNRILIEEKCTINHGAIGNOAHN	718
Oy	382	VIVAPSSHNKYGAESEFPGLIYDALDFIESKVDPDSKAMGDVKRISVAAFVPOAA	434
Dd	719	VLFHESPDMWDGDAISOYHDIKSITSNTD-SKELGKSLROLAKITALYVNA	770

RESULT 5			
08HZV3			
ID	08HZV3	PRELIMINARY;	PRT; 768 AA.
AC	08HZV3;		
DT	01-MAR-2003 (TREMBLrel. 23, Created)		
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Transferlin receptor.		
GN	TRFC.		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.		
OX	NCBI_TaxID=9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Small Intestine;		
RA	Python P., Jorg H., Neuenschwander S., Stranzinger G., Vogeli P.;		
RT	"The complete cDNA sequence of porcine transferlin receptor gene.";		
RL	Submitted (SEP-2001) to the EMBL/Genbank/DBD databases.		
DR	EMBL; AF416763; AA09749.1; -.		
KW	RECEPTOR.		
SO	SEQUENCE	768 AA;	86121 MW; 55B1SCFA2F4D1CF CRC64;

Query Match	17.8%	Score 415.5	DB 6	Length 768
Best Local Similarity	24.7%	Pred. No. 3.1e-23		
Matches	112	Conservative	90	Mismatches 169; Indels 83; Gaps 12

QY	10	SWRGSLSKYSVNGPFGTGNFSTQYKMMHLSHNEVTRYIYVIGTLGAVEPRRYVLGGH	69
Db	364	TWRTEFPCKLVSSP-----SKNKLTVNNVLKELIKILINFGVIGFEEDPRVILGAQ	416
QY	70	RDSWTFGGIDPQSGAAVYHEVYKRSCTLKEG-WRRRTITLASMDAEFGLLSGTSEMAE	128
Db	417	RDAMVPGAKRSVGSVSLNLINLAQILLSDMYIKQFNPRSRISVPAWSAGFGAIGAEWLE	476
QY	129	DNSRLQERGVAIYIADSSIEGNYTLRVDCETPLMKSLVYNTLKEKLSPEDEGKSLY--	186
Db	477	GYLSSLHKAFTYINLKDRAVLGTSNPKFVASPDLTSLIEKMMQDVNP--VTGGSLTYND	533
QY	187	ESWTKK-----SPSPFSGMRLSKLGSQNDVEVFEORLGIASGRARYTKMETN	236
Db	534	SNMIVKVEKLSHDDAFAFPFLAYSQIPAAVS-----	562
QY	237	KF-----SGYPLVSHVEFETYLEVEKFDPMKRYHLTVAQRGWAFELANSYLPEDCRD	291
Db	563	-FCCECDTIDYPLGLTMTIDYDLKSRVQNLNPMARAABVAAGHLYIKLTIDELNLN---	618

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OY 292 YAVLRKRYADKIYNISMKHPQ---EMKTYISLSPDLSFAVKNFTFIASKFSRRLDOPDKS 348
DB 619 -----YEMNDNLILSVREMNQFRVDIREMGLSLQWLYSARQDFFRATSRILSDYNNVETR 674
OY 349 NPILRRMNNDOLMFLERAFIDPLGIDRRPFYRHVYAPSSHNKYAGESFPGIYDALPDI-I 407
DB 675 DKFWREIRLIMKEVYHFLSPYSPRESFRRHITWGSGRH-----LSALVEHL 724
OY 408 ESKVDPSKMGD--VKROIISVAALFTVQAAETLS 439
DB 725 KLRKRNSSAFNOTLKLQALATWTIOGAANALIS 758

RESULT 6
OY 094JH4 PRELIMINARY; PRT; 621 AA.
AC 094JH4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Peptidase-like protein.
GN P0638D12.15.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GN3) genomic DNA, chromosome 1, PAC
clone:p0638D12."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002972; BAB55507.1; -.
DR Gramene; O94JH4; -.
DR InterPro; IPR003137; PA.
DR Pfam; PF02325; PA; 1.
DR Pfam; PF04253; TPR_dimer; 1.
DR PROSITE; PS50840; PA; 1.
DR SEQUENCE 621 AA; 67139 MW; 8D471DA2259016A4 CRC64;

Query Match 17.7%; Score 412; DB 10; Length 621;
Best Local Similarity 24.2%; Pred. No. 4.2e-23;
Matches 111; Conservative 63; Mismatches 116; Indels 168; Gaps 12;
OY 1 MGSAPPDSSNRG-SLKVSYNWGP-----FTGNSTQVKKMHISTNEVTRIYVIG 52
DB 309 LGGDAAP-ADMQREGSPVYRLGPPAILNLTYGN-----DMATLENVFA 354
OY 53 TLKRAVEDPRVILIGHRDWNFGGIDPQSGAAVYHETVNSFGTLKKGMRPRRTILFAS 112
DB 355 VIEEAEEPRVILVIGNHRDAMTFGASDPNSGTAMIEAQLSLVLOKQGMPPRTIIFCS 414
OY 113 WDAEEFLLGSTWAEDNSRLQERGAAYIADSSIEGNTLARDCTPIIMSLYNNLTKE 172
DB 415 WDAEEYGL----- 422
OY 173 LKSPDEGFEEKSLYESWTKSPSPFGMPRIKSLGSGNDFEYFORLIASGRARYTK- 231
DB 423 VQPDN--SSQAVYDSWVKSNIPLDQAIPI-----IRYTM 458
OY 232 --NMETKKSFGYPLIYSHVETVELVEKPYDPMERKHLTVAOVRGMVFELANSIVLPDC 289
DB 459 SCGRNSEEIIG----- 469
OY 290 RDVAVVLRKYADKIYNISMKHPQEMKTYISLSPDLSFAVKNFTFIASKFSRRLDOPD--- 346
DB 470 --SVGTLOATTKYVEN-----EVKGTALSCSPDLHNAIRALKTAATKVGKEREIROL 520
OY 347 -----KSNPILRRMNNDOLMFLERAFIDPLGIDRRPFYRHVYAPSSHNKYAGESFPGIY 401
DB 521 SSNQLKDKSMKIRSLNRLMQAERAFINRBSGLFKREMFKLIVYGPSEQNDMESASTYGEV 580
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OY 402 DALFDIESKVDPSKMGDVKKROIISVAALFTVQAAETLS 439
DB 581 NAIASAR-KENTTESMKRVQEHHRVARATIQASVILA 617

RESULT 7
OY 08LO61 PRELIMINARY; PRT; 298 AA.
AC 08LO61;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Putative peptidase-like protein.
GN P0439E07.19.
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (Japonica cultivar-group) genomic DNA, chromosome 1, PAC
clone:p0439E07."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003768; BAB91937.1; -.
DR Gramene; Q8LO61; -.
DR SEQUENCE 298 AA; 33607 MW; 5051AC94C99C5BD3 CRC64;

Query Match 17.4%; Score 404.5; DB 10; Length 298;
Best Local Similarity 30.6%; Pred. No. 5.4e-23;
Matches 101; Conservative 69; Mismatches 111; Indels 49; Gaps 9;
OY 121 LGSTWAEEDNSRLQERGAAYIADSSIEGNTLRVCTPLKMSLYNNLTRELKSPDEGF 180
DB 3 VGSTEWEEENKAMLTSTRYAVLVNDASAVYG-AGFYASATPOLDELLKEASKOVONPN-- 59
OY 181 EGSLSYESTWKTKSPSPFGMPRIKSL-GSGNDFEYFORLIASGRARYTKMNETKFS 239
DB 60 ETQSLVDLM-----ASDSSSMIKRIGRGSGSDYSAVQIHGIPS-----IDISMG 107
OY 240 GYPLIYSHVETVELVEKPYDPMERKHLTVAOVRGMVFELANSIVLPDCRDVAVVLRKY 299
DB 108 EYAVYHSLYDDFVWMEKFCPLFRRHVAASMGVLALRLSDEEILPEFNSTYAAVELEKG 167
OY 300 ADKIYNISMKHP-----QEMKTYISLSPDLSFAVKNFTFIASKFSERLDPKSN 349
DB 168 AIDINKRLGVPSSSPLQKSIAEFKRAALQMDSEMKALQ-----TRKWNPNRRN 218
OY 350 PILLRRMNNDOLMFLERAFIDPLGIDRRPFYRHVYAPSSHNKYAGESFPGIYDALFDIES 409
DB 219 PLKRVDLNERLIMTERAFTIREGLSGRPWKHLVY-----PGVDAT- QMAE 264
OY 410 KVDPKAMGDVKKROIISVAALFTVQAAETLS 439
DB 265 RTNTESEMSRVSQHEIYRIARVINOASLVLS 294

RESULT 8
OY 094JH3 PRELIMINARY; PRT; 606 AA.
AC 094JH3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Peptidase-like protein.
GN P0638D12.16.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
```

Query	Subject	Score	Length	Mismatches	Indels	Gaps
QX	NCBI_TaxID=4530;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=cv, Nipponbare;					
RA	Sasaki T., Matsumoto T., Yamamoto K.;					
RT	"Oryza sativa nipponbare(Ga3) genomic DNA, chromosome 1, PAC					
RT	clone:p0638012."					
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.					
DR	EMBL, AP002972; BAB55508.1; -					
DR	Gramene; Q94JH3; -					
DR	InterPro; IPR001337; PA.					
DR	Pfam; PF02225; PA; 1.					
DR	Pfam; PF04253; TFR.dimer; 1.					
DR	PROSITE; PS50840; PA; 1					
SO	SEQUENCE 606 AA; 65594 MW; F80DDCBF731058B6 CRC64;					
Query Match	15.2%; Score 353.5; DB 10; Length 606;					
Best Local Similarity	22.4%; Pred. No. 1,3e-18;					
Matches	100; Conservative 47; Mismatches 82; Indels 217; Gaps 10					
QY	1 MGSAPPDSSNRGSLKV-SYVNGP-----FTGNFSTQVKMHIHSTNEVTRYIYVIG 52					
DY	321 MGSAAAP-TEWQGGEGAPMYRLGCGPAVLNLTLYIGN-----DLTATENVFA 366					
QY	53 TLRCGAVEPDRVYIIIGHHDSWVFEGIDPQSGAAVYHETVRSFGTLKKGWPRRTILLAS 112					
DY	367 VIEKKEEDRVYIIIGNHRDAWTFGAIVDPSNSTAAMLTAERLSKLEKKGWPRRTIIVCS 426					
QY	113 WDAEEFGILGSTEWAEDNSRLQERGVAYINADSSIEGNTYLRVDCPTLMVSLVYNIKE 172					
DY	427 WDAEEFPL- 434					
QY	173 LKSPDEGEFGKSLYESMTKSPSEFGSGMPRIKSLGSGNDEVEFQRLIASGRARYTKN 232					
DY	435 VQDDDD-----PS----- 442					
QY	233 WETKFKSGPIYHSHVETVELYKEFYDPMFYTHLTVAGVREGMVFELANSIYLPFDCCDY 292					
DY	443 -----QTLDTMIGHHPMLQ-----AENW 462					
QY	293 AVVLRKYADKIYINISMKNPQEMKTYSLSFDSLFSAVKNFTELASKFSRLQDFDKSNPL 352					
DY	463 SLKTRATYVY----- 473					
QY	353 LRMNDQLMFLERAFIDPLGLPDRPFYRHVITYAESSHNKYGSESPGCIYDALFDIESKVD 412					
DY	474 -RDINDRLMAEREFINREGIDSGRPWKHKMIIYASSDDQDDMTKAFPGIVSAI-DKANRKN 531					
QY	413 PSKMGVDYKQIISVAFTVQAAETL 438					
DY	532 TTESWOLIQHEIYRARAARAVSKASAVL 557					

```

RN      [12]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Columbia;
RA      Joshu C., Bauer C., Holic M.;
RT      "The sequence of A. thaliana F10A2.";
RL      Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN      [13]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Columbia;
RA      Waterston R.;
RL      Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN      [14]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Columbia;
RA      Waterston R.;
RL      Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN      [15]
RP      SEQUENCE FROM N.A.
RC      STRAIN=cv. Columbia;
RA      Waterston R.;
RL      Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN      [16]
RP      SEQUENCE FROM N.A.
RC      EU Arabidopsis sequencing project;
RA      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF147259; AAD29787.1; -
DR      EMBL; AL161506; CAB81137.1; -
DR      HSSP; P02786; ICX8.
DR      InterPro; IPR003137; PA.
DR      Pfam; PF02225; PA; 1.
DR      PROSITE; PS50840; PA; 1.
SQ      SEQUENCE   280 AA; 3115 MW; AB7EFCFE1870386 CRC64;

Query Match          10.8%; Score 252; DB 10; Length 280;
Best local similarity 45.5%; Pred. No. 2,5e-11;
Matches 51; Conservative 16; Mismatches 27; Indels 18; Gaps 3

QY      20 NVGPGFTGNSTOKVKKHHTSTNEVTIRIYNIGTLRGAVEBPDRIYLGGHRDSWFGGD 79
DY      147 DVGPG-GGILNLSTY-----VTKIQNVIGIEGEEDPRIVILNNHRDTTFRAVD 196
BY      80 PQSGAAVHVHEVRSE-----GLTKEGRNRPRTITLFASMDAEFFLGGS 123
DB      197 PNSGTAVLMESKSYLQHIAQRDLKLQKRWKPRRTITLCWMDAEYGLVSS 248

RESULT 10
Q08693 PRELIMINARY; PRT; 809 AA.
AC      Q08693;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Chromosome XV reading frame ORF YOR256C.
GN      YOR256C.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC      Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX      NCBI_TaxID=4932;
RX      [1]
RP      SEQUENCE FROM N.A.
RA      MIPS;
RL      Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE-97298311; PubMed-9153759;
RA      Uunaux J.C., Potley R.;
RT      "Sequencing analysis of a 36.8 kb fragment of yeast chromosome XV
RT      reveals 26 open reading frames including SEC63, CDC31, SUG2, GCD1,
RT      RIL2, PNI1, PAC1 and VPH1.";
RL      Yeast 13:483-487(1997).
EMBL: Z75164; CA99478.1; -.
SDD: S0005782; YOR256C.

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DR InterPro; IPR003137; PA.
DR Pfam; PF02225; PA; 1.
DR Pfam; PF04253; TFR_dimer; 1.
DR PROSITE; PS50840; PA; 1.
DR SEQUENCE 809 AA; 91995 MW; D7D68C0A8C50ECB2 CRC64;
Query Match 10.3%; Score 240.5; DB 3; Length 809;
Best Local Similarity 22.4%; Pred. No. 9.2e-10;
Matches 98; Conservative 78; Mismatches 160; Indels 101; Gaps 19;
47 IYNYGTLRGAVPEPRVYILGHRDSWFGIDPQSGAAVYHETVRSFGTLK-KEGMRPR 105
423 IPNIVGKIEGRQSKAIIIIASRNSINFGTTPYFNGAIIISYQLFOEYVKFGKMRPL 482
106 RTILFASMDAEFFGLGSTEMAEDNSRLLOER-----GVAYINADSSIEGNTYLR 155
483 RNIVFLISGCGTEFNYAGSELSIEORLTPLKDEIVSLIDISOLGIPFAEKYENGKTRGELS 542
156 VDCPTPLMSLVYNLTKELKSPDEGFKSLYESWTKKSPSPF-SGMPRISKLSGDNFE 214
543 IETHPLLKRF-FNRNNAH-GNFDISVNDVOHYGDMT-----PFLANGIP-VSYISSD---- 590
215 VEFORLIASGRARYTKNWEIKNKFSGYPLYSVETVELVEFYDP-----MFK 263
591 -----STNNRDTPT-ETSE-----DKFERVEKILEDEQNOQSVKDLLVYL 629
264 YHLTYAOVGKGVFELANSIVLPDCRDYAVYLKADKIYINSMKHPOEMKTYSLSPDS 323
630 LHISM-----ELIDPLLHFIDILSY---VEDIDERLQRLQOAYPEK-----LNFTS 672
324 LFSAVNFEIISKESERLODF-----DKSNPILRM---AMDOLFEERAFIDPL 371
673 IIRGLLEFWKIGSEWASWTOGWNENIYWSHGDGIEPILSLINRTYKTKLLINIRGCSPA 732
372 GLDPRFPRVHVIYAPS-----SHNKYAGE---SFGPIYDALPDIESKVDPSKAGDYKRQ 423
733 GLPNRSEFYKVLGCPILIOEDKSKNGVDFMTFPGVMAIYDD-----WKRAQEQ 784
424 ISVAALFTVQAALFTLSE 440
785 IDLIGKVLHQSAAFLVE 801
Db
RESULT 11
08C872 PRELIMINARY; PRT; 515 AA.
08C872 AC
01-MAR-2003 (TREMBLrel. 23, Created)
01-MAR-2003 (TREMBLrel. 23, Last sequence update)
01-MAR-2003 (TREMBLrel. 23, Last annotation update)
Transferin receptor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA THE FANTOM Consortium;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RT Nature 420:563-573(2002).
RL EMBL; AK048228; BAC33277.1;
DR SEQUENCE 515 AA; 57341 MW; 86FC77FF66A80DDF CRC64;
SO
Query Match 9.6%; Score 224.5; DB 11; Length 515;
Best Local Similarity 34.6%; Pred. No. 8e-09;
Matches 55; Conservative 31; Mismatches 52; Indels 21; Gaps 6;
1 MGSAGP-----DSSWMSGLKVSYNVNGPFTGNFSTQKMKMHSTNEVTRIYNVIGTLRG 56

Db 351 MEGSPARWINDSCK--LELSON-----QNVKLIVKVLKERRILNIFGVING 397
Oy 57 AVEEDRVYILGHRDSWFGIDPQSGAAVYHETVRSFG-TLKEGMRPRRTILFASW 113
Db 398 YEEDRVYVVAQDA-LGAGVAAKSSVGTGLTLKLAQVSDMTSKDGFSPRSIIIFASW 456
Oy 114 DAEEFGLGSTEMAEDNSRLLOERGVAYINADSSIEGNY 152
Db 457 TAGDGAAGATEMLEGYLSLHLKAFYIINLDKVLGKH 495
Db
RESULT 12
008919 PRELIMINARY; PRT; 783 AA.
ID 008919
AC 008919;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Chromosome XVI reading frame ORF YPL176C.
GN YPL176C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Nentwich U., Voss H., Ansgore W.;
RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RA MIPS; Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
RL EMBL; Z73532; CA97883.1;
DR SGD; S0006097; YPL176C.
DR InterPro; IPR003137; PA.
DR Pfam; PF02225; PA; 1.
DR Pfam; PF04253; TFR_dimer; 1.
DR PROSITE; PS50840; PA; 1.
DR SEQUENCE 783 AA; 86735 MW; 85D78D5D2FEL1AA7 CRC64;
SO
Query Match 7.7%; Score 179.5; DB 3; Length 783;
Best Local Similarity 19.7%; Pred. No. 4.2e-05;
Matches 93; Conservative 82; Mismatches 169; Indels 127; Gaps 20;
Oy 15 LKVSYNVNGPFTGNFSTQKMKMHST-NEVTRIYNVIGTLRGAVPEPRVYILGHRDSW 73
Db 374 VKFSNLT---FSGSLNDCRLDLVOTAIRERHPVHDVIGTIEGSEQAGRAIVLAAPNSA 430
Oy 74 VFGGIDPQSGAAVYHETVRSFGTL-KEGMRPRRTILFASMDAEFFGLGSTEMAEDNSR 132
Db 431 SYGTWPSFGIVVLSLIQLQENVYKFDMPKLANIYFISFGSEFENAGATELMEKRT 490
Oy 133 LLOERGVAYINA-----DSSIEGNTYLRVCTPLMYSLVYNLTKELKSPDEGFEKSL 185
Db 491 ALKSEIYTIIDVGIGIWDSON-----NLEIQCHPLLVDL---FQKNMTSKENKVDNV 542
Oy 186 YE--SWTKKSPSPFS-GMP--RISKLSGNDPEVVF---QLGIASGRARYTKNWEIKN 237
Db 543 HQFGDMT-----PYLAQIPVAILISSPCVMNRREHPYIYVEKPFIDKLADKKKGEV-- 595
Oy 238 FSGYPLYSVETVELVEKFPDPMFKYHLFVAQVGGVAFELANSIVLPDCRDYAVYLR 297
Db 596 LSEIMLY-----LVK-----SLDLIDDPFIPFISINVDL- 627
Oy 298 KYADKIYINSMKHPOEMKTYSLSPDSLSAVKNFELASKSERLODFKSNPILLRMN 357
Db 628 -----STILKDLQKECPDYVNFDEVLGTTLWENTKLOPEKMKSEW----- 668
Oy 358 DQMLFERAFIDPL-----GLDPRFPRVHVIYAPS SHNKYA 393
Db 669 TELMWGAGYIEPTILAIINRSMWNLISLIGVTOCLEGLEDKDRFTYKKNVIGPKIM----- 724
Oy 394 GSEPGIYDALPDIESKVDPSKAW--GDVKKRISVAALFTVQAALFTLSEV 441

Db 725 -----VDKCDPLRSWTFPEIRDTIAIKDMSVQVQANTLGTI 761

RESULT 13

ID 09PF58 PRELIMINARY; PRT; 529 AA.

AC 09PF58; 09PF58;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein Xf0820.

GN Xf0820.

OS Xylella fastidiosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xylella.

OX NCBI_TaxID=2371;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=9a5c;

RX MEDLINE=20365717; PubMed=10910347;

RA Simson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Boye J.M., Britones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorriy H., Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Fraga J.S., Franco S.C., Franco M.C., Fromme M., Furlan L.R., Gardier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitaajima J.P., Krüger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.J., Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Machado M.A., Madeira A.M.B.N., Martins E.M.F., Matsukuma A.Y., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.F.M., Miraca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H., Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C.;

RT "The genome sequence of the plant pathogen xylella fastidiosa.";

RL Nature 406:151-159(2000).

DR EMBL: AE003921; AAF83630.1; -

DR InterPro: IPR000010; Cyscatin.

KW Prosite: PS00287; Cyscatin; 1.

KX Hypothetical protein: complete proteome.

SQ SEQUENCE 529 AA; 57664 MW; 37EFC71953B41655 CRC64;

Query Match 7.4%; Score 173; DB 16; Length 529;

Best Local Similarity 31.1%; Pred. No. 7.5e-05;

Matches 66; Conservative 30; Mismatches 70; Indels 46; Gaps 11;

QY 42 NEYTRIVNIGTLRGAVPEDRYVILGGH-----SNWF-GGIDPOSGAAVHE 89

Db 270 SEVITSHNVAAALGGCAHPDETVIYSAHMDHIGVGPDAKGTIFENGALDMSGTAALLE 329

QY 90 TVRSFGTLKKBEGRPRTTLFASMDAEEGLGSPFMADNSRLLOERVAITINAD---- 145

Db 330 LARGFA-----KGPQPORSVLFLAVTAEEGLGGS--EYVANSPLVLEKTVAAVINMDVNP 384

QY 146 ---SSIEGNY-ILRVDCPTLM-----YSLVYNLTKELKSPDEGFGKSLYSWTKSSPS 195

Db 385 QGPTBDFGIYGAKLDDMLKQVAAGWKLRYTLD---PTPEAGHFRSDHRSFAAR---- 438

QY 196 PEPGMPRIKSLGSGNDFEVFFORUGIASGRA 227

Db 439 ----GIPALS-YSAGODMEVG----GVAAGKA 461

RESULT 14

ID 08P530 PRELIMINARY; PRT; 549 AA.

AC 08P530;

DT 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Aminopeptidase.

GN XCC3517.

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=340;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33913 / NCPPB 528;

RX MEDLINE=22022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorriy H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A., Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spínola L.A.F., Takita M., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitaajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";

RL Nature 417:459-463(2002).

DR EMBL: AE012471; BAM42787.1; -

KW Complete proteome.

SQ SEQUENCE 549 AA; 59295 MW; B6FB8307A172C071 CRC64;

Query Match 6.8%; Score 158; DB 16; Length 549;

Best Local Similarity 26.2%; Pred. No. 0.0011;

Matches 59; Conservative 33; Mismatches 61; Indels 72; Gaps 10;

QY 42 NEYTRIVNIGTLRGAVPEDRYVILGGH-----RDSNWF-GGIDPOSGAAVHE 89

Db 291 SPVITSHNVAAALGGCAHPDETVIYSAHMDHIGVGPDAKGTIFENGALDMSGTAALLE 350

QY 90 TVRSFGTLKKBEGRPRTTLFASMDAEEGLGSPFMADNSRLLOERGVAVITINAD-- 145

Db 351 LARGFA-----KGPKEPRSVFLAVTAEEGLGSEFYA---SKPLPLATVVAVINMDGM 403

QY 146 ---SSIEGNYTLRVDCPTLMYSLVYNLTKELKSPDEGFGK 182

Db 404 NPFVPSRDGIYGTAKLELLDQKTVAGQWKLRYTPD-----KPEAGYFF 449

QY 183 KSLYESWTKSSPSPGMPRIKSLGSGNDFEVFFORUGIASGRA 227

Db 450 RSDHRSFAAR-----GVPALS-YAAGODMEVG----GVAAGKA 482

RESULT 15

ID 09A5A8 PRELIMINARY; PRT; 467 AA.

AC 09A5A8;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Aminopeptidase, putative.

GN CC2544.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=112559647;
RA Niernmen W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL: AE005922; AAK24515.1; -.
DR TIGR: CC2544; -.
DR InterPro: IPR003137; PA.
DR PROSITE: PS50840; PA: 1.
KW Complete proteome.
SQ SEQUENCE 467 AA; 48918 MW; 9984DE2A9D84F00F CRC64;

Query Match 6.7%; Score 157; DB 16; Length 467;
Best Local Similarity 30.3%; Pred. No. 0.0011;
Matches 44; Conservative 28; Mismatches 59; Indels 14; Gaps 6;
OY 30 STOKVKMHI-----HSTNEVTRIVNIGTLRGAVEPDRVILGGHRSWF--GGIDPQS 82
DB 232 AARKVPRVKLKLESSVNPNNVAMNISGDIKGSEKPDVEIYIGGHLDSWDVGTGALDDAT 291
OY 83 GAAVYHETVRSFGTLKKKGWRPRRTILFASWDAEFEGLLGSTE-WAEDNSRLQERGVAY 141
DB 292 GIATTTAAKLIQDLPK--RPKRTIRVVMWGSESG--GSSEAYLAANKDALSTMVLG 346
OY 142 INADSSIEGNTLRVDCITPLMYSLV 166
DB 347 -ESDPTGADRIYSIQVPAAGSLDHPV 370

Search completed: October 4, 2003, 23:25:13
Job time : 81 secs